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Slobodyansky, Elizabeth

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Elizabeth Slobodyansky, PhD

Primary Examiner

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NA Sequence: #_______

AA Sequence : #_______

Structure: #______

Bibliographic:

Litigation:

Patent Family:

Other:

Vendors and cost where applicable
STN: _____
DIALOG: ____
QUESTEL/ORBIT: ____
LEXIS/NEXIS: ____
SEQUENCE SYSTEM: ____

WWW/Internet:_____Other(Specify):_____

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OM protein - protein search, using sw model

August 5, 2004, 13:09:29; Search time 54 Seconds (without alignments) 617.419 Million cell updates/sec Run on:

US-09-430-029-8 Perfect score:

619
1 MDAGRVCGTVTIAQTDERYA......RLRKPFFCGMACAGTAAINK 118 Sequence:

BLOSUM62

Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1586107 seqs, 282547505 residues Searched:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

A_Geneseq_29Jan04:* 1: geneseqp1980s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp1980s:* geneseqp1990s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

STIMMADIES

	Description	A CONTRACTOR OF CONTRACTOR CONTRA		AACCASA K. EULIOD		Aaw98976 Blosligen			Protein	Oxidage	Drotein	Protein	Sphinoon			Protein	Protein) 1	٠.	ָבֶּלְ בְּלָבֶ				Aar05385 Xylene ox	Abp97023 Pseudomon	œ	
SUMMAKIES	ID	AAY84822	AAY96262	AA023395	AAG64662	AAW98976	AAR66216	AAR81472	ABU22750	AAW80338	ABU21309	ABU19841	ABP97021	ABP97025	ABU41589	ABU40068	ABU38911	ABP79217	AAW14449	ABP78930	ABI13 73 5.3	on of contract	ABU229/3	AAR05385	ABP97023	AAB60228	AAG92388
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₩	Query	100.0	67.6	52.0	41.9	36.9	23.3	23.3	21.1	20.9	20.4	20.1	19.9	19.9	19.4	18.9	18.3	17.9	17.8	17.7	17.7	17 6		0.71		16.9	16.7
	Score	619	418.5	322	259.5	228.5	144.5	144.5	130.5	29	126.5	124.5	123	123	120	117	113	111	110	109.5	109.5	601) C) () () ()		\sim	103.5
	Result No.	Н	7	e	41	2	9	7	no 1	D	10	11	12		14			17	18	19	20	21	10	4 (57	77	25

Abu40855 Protein e Aab29472 Burkholde Abu31907 Drotein e			F-1	-		Abu21203 Protein e			Abu22741 Protein e	Abul5018 Protein e	Nove h		
ABU40855 AAB29472 ABU21907	ABU38023 ABU25632	ABR61631 ABU20107	ABP78834 ABU50056	ADA35088	ABU31645	ABU21203 ABU48037	AAY35534	ABU27042	ABU22741	ABU15018	AAU23193	AAY96261	AAW98975
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334 342 419	336 664	348 382	96 3 4 0	358	322	323	431	431	381	322	336	352	356
16.6 16.6 16.6	16.4	16.2	16.1 16.0	15.5	14.9	14.8	14.6	14.6	14.5	14.5	14.5	14.2	14.2
103 103 103	101.5 101	100.5	99.5 99	96	92.5	91.5	90.5	90.5	06.00	٠		88	88
26 27 28	30	31	3 3 4	32	9 6	- 80 n m	39	0 1	4.	2.4	43	44	45

ALIGNMENTS

RESULT 1 AAY84822

AAY84822 standard; protein; 118 AA.

AAY84822;

08-AUG-2000 (first entry)

Amino acid sequence of toluene monooxygenase TomQ.

Toluene monooxygenase; TomK; TomL; TomN; TomO; TomP; TomQ; toluene; ortho-cresol; 3-methylcatechol; chlorinated compound; aliphatic hydrocarbon; trichloroethylene; dichloroethylene; phenol; aromatic compound; benzene; cresol; environmental remediation.

Burkholderia cepacia.

EP999274-A2.

10-MAY-2000.

99EP-00121681. 02-NOV-1999;

98JP-00310801 30-0CT-1998;

(CANO) CANON KK.

Imamura T; Yano T, Nomoto T,

2000-306010/27. N-PSDB; AAA14845 Novel DNA fragment encoding a toluene monooxygenase, useful for degrading a chlorinated aliphatic hydrocarbon compound, or an aromatic compound, e.g. in environmental remediation.

Claim 46; Page 45; 52pp; English.

AAY84816-22 represent toluene monooxygenase enzymes TomK, TomL, TomM, TomO, TomP, and TomQ, respectively. The enzymes oxidise toluene to ortho-cresol and 3-methylcatechol. The toluene monooxygenase has a high cefficiency in degrading aromatic and volatile organic chlorinated compounds. The nucleic acids are useful for the recombinant production of toluene monooxygenase. Toluene monooxygenase is useful for degrading a chlorinated aliphatic hydrocarbon compound (e.g. trichloroethylene (TCE) or dichloroethylene (DCE)), or an aromatic compound (e.g. toluene, benzene, phenol, and cresol), e.g. in environmental remediation. It is especially useful for purifying air polluted with chlorinated aliphatic

68

Thu Aug

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Bramucci MG,
                                                                                                                                                                                                                                                                                            US6548292-B1.
                                                                                                                                                                                   06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the Ralstonia eutropha toluene monooxygenase TomO polypeptide. This peptide is encoded by a DNA fragment of about 5.3 Kb which also contains six other coding sequences encoding other toluene monooxygenase polypeptides (AA30292). The DNA fragment is useful for transforming microbial calls to confer them with toluene monooxygenase activity. These cells are in turn useful for decontaminating environments polluted with halogenated aliphatic compounds e.g. tetrachloroethylene (PCE), trichloroethylene (TCE) and dichloroethylene (DCE) and/or aromatic hydrocarbons e.g. toluene, benzene, phenol, cresol. These pollutents are considered to be potential carcinogens. The present sequence is not essential for toluene monooxygenase activity. (Updated on 12-SEP-2003 to standardise OS field)
                                                                  ô
                                                                                        1 MDAGRVCGTVTIAQTDERYACVSGESILAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide encoding toluene monooxygenase for generating transformants useful for decontaminating environments polluted with e.g.
                                                                                                           MDAGRVCGTVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAV 60
                                                                                                                                      RKLGPISRAHVSAEBENDGYALACRVVPDGDVELEVAGRLRKPFFCGMACAGTAAINK 118
                                                                                                                                                     Toluene monooxygenase; carcinogen; halogenated aliphatic hydrocarbon; halogenated aromatic hydrocarbon; environmental pollution; TomQ; environmental remediation; enzyme.
                                                                   Gaps
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0
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                                          100.0%; Score 619; DB 3; Length 118; 100.0%; Pred. No. 1.5e-63; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                            R. eutropha toluene monooxygenase TomQ polypeptide.
                                                                                                                                                                                                                            AAY96262 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 38; Page 48; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   Ralstonia eutropha; strain TB64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Imamura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         99EP-00124209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98JP-00344506
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Best Local Similarity 76.7
Matches 79; Conservative
                                                                                                                                                                                                                                                                                       (first entry)
                                                           Best Local Similarity 100.
Matches 118; Conservative
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                                                                                                                                                                                                                                                                            (revised)
hydrocarbon compounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nomoto T,
                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CANO ) CANON KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 111 AA;
                       Sequence 118 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                            EP1006191-A2
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                                                                                                                                                                                                                                                                           12-SEP-2003
11-SEP-2000
                                                                                                                                             61
                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yano T,
                                                                                                                                                                                                                 AAY96262
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Specifically, the plasmid pCT14 carries the genes necessary for replication and stability in a host, as well as genes encoding enzymes for the degradation of various aromatic substrates including catechols and other intermediates in the toluene degradative pathway. Furthermore, pCT14 carries heavy metal resistance genes and is useful for reducing the level of mercury in a contaminated environment. As for other bacterial plasmids, pCT14 also carries genes that are used for plasmid replication, partitioning of replicated plasmids to daughter cells during cells dispection and transposition of insertion sequences or transposons. This polypoptide sequence is the Pseudomonas pCT14 ORF1 ferredoxin protein, which reactivates the catechol dioxygenase enzyme encoded by ORF2 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TVTIAQTDERYACVSGESILAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
                                        Bacterial plasmid, CT14, aromatic degradation, heavy metal resistance; catechol, toluene degradative pathway, mercury; ferredoxin, ORF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New bacterial plasmid isolated from Pseudomonas CT14, designated as pCT14, useful for degrading aromatic compounds, and in plasmid replication, or partitioning of replicated plasmids to daughter cells during cell division.
TVTIAQTDERYACVSGESILLAGMAKLGRRGI PVGCLNGGCGVCKVRVLRGAVRKLGPISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 AHVSAEEENDGYALACRVVPDGDVELEVAGRLRKPFFCGMACAGTAAINK 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas plasmid CT14 ORF1 bacterial ferredoxin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35; Indels
                                                                                                                                69 AHVSAEBENDGYALACRVVPDGDVELEVAGRIRKPFFCGMACA 111
                                                                                                                                                                         52.0%; Score 322; DB 7;
llarity 56.4%; Pred. No. 3.6e-29;
Conservative 13; Mismatches 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Col 31-34; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                              Ä
                                                                                                                                                                                                                                                                                                                                                                              AAO23395 standard; protein; 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-2000; 2000US-00716865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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N-PSDB; AAL56814.
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Matches 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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Alkene mon:oxygenase and corresp. gene - useful for the epoxidation of an
                                                                                                                                                                                                                    - useful in the
                                                                                                                                                                                                                                                                       The present sequence encodes Alcaligenes sp. protein PoxG. The present invention also describes PoxB, PoxB, PoxC, PoxD, PoxE, PoxF, PoxR, and PoxI. The proteins are useful in the fields of pertroleum purification, chemical industry and drug industry related to the synthesis, conversion and decomposition of aromatic compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                     aromatic; oxidative; petroleum purification; chemical industry; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                   9 TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR
                                                                                                                                                                                                                                                                                                                                                                                                   ۲,
                                                                                                                                                                                                               New encoding an aromatic cpd. oxidative decompsn. enzyme – use.
fields of petroleum purification, chemical and drug industries
                                                                                                                                                                                                                                                                                                                                                                           Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alkene monoxygenase; reductase; epoxidation; amoD.
                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 AHVSAEEENDGYALACRVVPDGDVELEVAGRLRK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nocardia corallina reductase (encoded by amoD).
                                                                                                                                                                                                                                                                                                                                                                     36.9%; Score 228.5; DB 48.9%; Pred. No. 2e-18; live 12; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 7-19; 35pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR66216 standard; protein; 342
                                                                                                                              97JP-00200625
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                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                            WPI; 1999-197820/17.
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                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                    (TOFU ) TONEN CORP.
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                                                                                                                                                                                        N-PSDB; AAX18867
                                                                                                                                                                                                                                                                                                                                                Sequence 101 AA;
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                                 Alcaligenes sp.
                                                                                                                             25-JUL-1997;
                                                         JP11042088-A
                                                                                                      25-JUL-1997;
                                                                                16-FEB-1999
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04-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a Stenotrophomonas maltophilia (Xanthomonas maltophila) DNA sequence which encodes 9 proteins. The invention includes a method for the production of 7-hydroxyindol and 7-hydroxytryptophan in which a microbe carrying a fragment of the DNA sequence is capable of hydroxylating the 7-position of indol is cultured. The DNA is useful in a method for producing 7-hydroxyindol and 7-hydroxytryptophan which are useful as raw materials for drugs, dyestuffs and reagents. The present sequence represents a protein encoded by the DNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                 New Xanthomonas maltophilia DNA sequence, useful in a method for producing 7-hydroxyindol and 7-hydroxytryptophan which are useful as raw materials for drugs, dyestuffs and reagents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                Xanthomonas maltophila; 7-hydroxyindol; 7-hydroxytryptophan; drug;
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 AHVSAEEENDGYALACRVVPDGDVELEVAGRIRKPFF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 259.5; DB 4;
Pred. No. 5.7e-22;
Trans 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 16; 23pp; Japanese.
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                                                                          112
                                                                                                                                            Hydroxyindol-related protein #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 101
                                                                                                                                                                                                      Stenotrophomonas maltophilia.
                                                                                                                                                                                                                                                                             99JP-00273961.
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                                                                     AAG64662 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp. protein PoxG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Conservative
                                                                                                                                                                                                                                                                                                                        (SAOC ) MERCIAN CORP
                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-370201/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW98976 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH45588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 112 AA;
                                                                                                                                                                                                                              JP2001095577-A.
                                                                                                                                                                                                                                                                            28-SEP-1999;
                                                                                                                                                                                                                                                                                                   28-SEP-1999;
                                                                                                                    14-SEP-2001
                                                                                                                                                                                                                                                    10-APR-2001
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             20
                                                                                              AAG64662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW98976;
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                                                          AAW98976
ID AAW9
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DT 10-M
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            qq
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68 61 4 ;

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276 alkene mono-oxygenase gene. The gene encodes 4 protein products amoh, amoB, amoC and amoD derived from the 3 different reading frames of the operon. The gene is useful for the production of indole. Nocardia corallina can be cultured in a medium cong. indole will readily oxidise the indole yielding indigo into the culture medium. B. coli may also be transformed with the alkene mono-oxygenase gene and used as above to efficiently produce indigo by microbial oxidation. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR81469-R81472 are protein products of the Nocardia corallina strain B-
                                  E.coli transformed with the DNA sequence AAQ79569 are able to catalyse the epoxidation of alkenes. The DNA is derived from Nocardia corallina and comprises 4 open reading frames. ORFs amoA and amoC encode subunits 1 and 2 of the alkene monoxygenase enzyme and ORF amoD encodes a reductase capable of transferring electrons from NADH coenzyme to a monoxygenase. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                  9 TVTIAQIDERYACVSGESILAGMAKLGRRGIPVGCINGGCGVCKVRVLRGAVRKLGPISR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of indigo by a microbiological method - by culturing a microbe alkene monoxigenase activity to oxidise indole to indigo.
                                                                                                                                                                                                                                                                                                  TINVQPFSHEYSCEDGESLLDG-ALRNSLLLKYGCKHGGCGTCKVRLLDGDVEEPGS-SF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        indole; indigo production; biosynthesis;
                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nocardia corallina alkene mono-oxygenase gene product, amoD.
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                               | : || : || | || || || ALTPEDREND-VILACASVPLEPCTIDVEPSGLTEEEFFSG 100
                                                                                                                                                                                                                                                                                                                                         AHVSAEEENDGYALACRVVP--DGDVELEVAGRLRKPFFCG 107
                                                                                                                                                                                                23.3%; Score 144.5; DB 2; 38.6%; Pred. No. 4.6e-08; iive 13; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laim 5; Page 8-9; 11pp; Japanese.
            Claim 2; Page 4-5; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gordonia rubripertinctus; B-276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR81472 standard; protein; 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94JP-00179688.
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                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microbial oxidation; dye.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alkene mono-oxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NIHA ) JAPAN ENERGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-133426/14.
                                                                                                                                                                                                                      Best Local Similarity
Matches 39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT17418
                                                                                                                                                                       Seguence 342 AA;
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07-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR81472;
                                                                                                                                                                                                                                                                                                                                              69
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 naving
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X X X D D D D D D X X X
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DB 2; Length 342;

Score 144.5; DB 2 Pred. No. 4.6e-08;

23.3%;

Query Match Best Local Similarity

9

Gaps

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the 6213 antiseases co an isolated nucleic acid comprising any one of the 6213 antisease sequences given in the specification where expression of the 6213 antisease sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid conclude whose expression is inhibited by the antisease concluded are:

(2) a host cell containing the vector; (3) an isolated nucleic acid; (2) a host cell containing the vector; (3) an isolated or its fragment whose expression is inhibited by the antisease nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the complete containing the polypeptide; (6) inhibiting cellular to proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway or the proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the extent or strains; or (13) identifying the carget of a compound that inhibits the extent or collection of an organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                     TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR
                                                                          TINVQPFSHEYSCEDGESLLDG-ALRNSLLLKYGCKHGGCGTCKVRLLDGDVEEPGS-SF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zyskind JW;
Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlsen KL,
Forsyth RA,
44; Indels
                                                                                                                        AHVSAEBENDGYALACRVVP--DGDVELEVAGRLRKPFFCG 107
                                                                                                                                                               ALTPEDREND-VILACASVPLEPCTIDVEPSGLTEEFFSG 100
                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #8277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; SEQ ID NO 50674; 1766pp; English.
    13; Mismatches
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                                                                                                                                                                                                                                                                             ABU22750 standard; protein; 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00946993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0352699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2002; 2002WO-US009107.
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      39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burkholderia mallei
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          Matches
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us-09-430-029-8.rag

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drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. auxeus, S. typhimurium, the remained for proliferation in cells other than S. auxeus, S. typhimurium, the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an oxidase which is derived from a microbe and converts a heteropolycyclic aromatic hydrocarbon to a benzoic acid homologue. The oxidase is used in a method for the removal of dioxin in which dibenzo-p-dioxin is converted to a diphenyl ether triol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 VTIAQTDERYACVSGESLLAGMAKLGRRGIPVGÇLNGGCGVCKVRVLRGAVRKLGPISRA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidase gene derived from a microbe for removal of dioxin - converts hetero:poly:cyclic aromatic hydrocarbon to a benzoic acid homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                           21.1%; Score 130.5; DB 6; 33.7%; Pred. No. 1.9e-06; ive 19; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVSAEEENDGYALACRVVPDGDVEL---EVAG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 12-13; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW80338 standard; protein; 329 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97JP-00084401.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97JP-00084401
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Best Local Similarity 33.7%
Matches 31, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-575906/49.
                                                                                                                                                                                                                                                                                                                                        Sequence 343 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP10257895-A.
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AC AAWE

AC AAWE

DT 12-C

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CVSGESILLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRAHVSAEEENDGY 80 14 CGSGKSLLVSALANG-IGFPYBCASGGCGVCKFELLEGNVQSMMPDAPGLSSRDREKGNR 72

81 ALACRVVPDGDVELEVA 97

Gaps

1;

Indels

Length 329;

20.9%; Score 129.5; DB 2; 39.0%; Pred. No. 2.4e-06; ; Pred. No. 2.4e-06; 11; Mismatches 35;

30; Conservative

21

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Local Similarity

Query Match Matches

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sectivity; (11) a culture computation of the strains is present in a culture or collection of compound activity; (11) a culture computing strains in which the extent compound that inhibits proliferation of the strains is present in a culture or collection of conduct is overexpressed or underexpressed; (12) determining the extent compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are useful for cell cellular proliferation of solate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #6836.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 49233; 1766pp; English.
                                                                                                                                  Ä
                                                                                                                              ABU21309 standard; protein; 343
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Carr GJ,
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2001US-00948993.
2001US-0342923P.
2002US-00072851.
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73 HLACQCVALSDLRIKVA 89
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                                                                                                                                                                                                                                                                                                                                          Burkholderia fungorum.
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Trawick JD,
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25-OCT-2001;
08-FEB-2002;
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                                                                                                                                                                      ABU21309;
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Wall D,
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substrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid;

(2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a compound that influences the activity of identifying a gene in inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                         Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                        10 VIIAQIDERYACVSGESILAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind JW;
Xu HH;
                                                                                    Gaps
                                                                                   13;
                                                              Length 343;
                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen Forsyth F
                                                                                                                                                                                                                                                                                                                    Protein encoded by Prokaryotic essential gene #5368
                                                                                    34;
                                                              DB 6;
                                                                                                                                                          98
                                                                                                                                                                                 94
                                                           20.4%; Score 126.5; DB 6 ilarity 35.4%; Pred. No. 5.5e-06; Conservative 15; Mismatches 34
                                                                                                                                                           ----VSAEEENDGYALACRVVPDGDVEL---EVAG
                                                                                                                                                                         Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 47765; 1766pp; English.
in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                            ABU19841 standard; protein; 343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
06-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001US-00815242.
                                                                                                                                                                                                                                                                                            19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-029926/02
                                                                      Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                     Borrelia cepacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ACA23711.
                                       Sequence 343 AA;
                                                                                                                                                                                                                                                                                                                                                                                             WO200277183-A2.
                                                                                                                                                            70
                                                                                                                                                                                                                                                                      ABU19841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang L,
Wall D,
                                                                Query Match
                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                   ABU19841
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or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense mucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational cut gascovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the property of the printed specification, but was obtained in electronic tother directs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||: |: :: | |::: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |
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oxidation; biocatalytic; xylM; xylM; 4-hydroxymethylbenzoic acid; film;
3-hydroxymethylbenzoic acid; p-toluic acid; p-tolualdehyde; polyester;
4-methylbenzyl alcohol; m-toluic acid; 3-methylbenzyl alcohol; fibre;
on which the test compound that inhibits proliferation of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 HVSAEEENDGYALACRVVPDGDVEL---EVAG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 ALSNDERTRGLALLCCSKAQCDLEIDVREIAG 94
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Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-354403/33.
N-PSDB; ACC49113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 343 AA;
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The present invention describes a method for oxidising a substituted monocyclic aromatic substrate (I). The method involves contacting a recombinant microorganism comprising a DNA fragment encoding a xylene monocygenase enzyme comprising a xylA subunit and a xylM subunit, with (I), or contacting a xylene monocygenase enzyme comprising a xylA subunit and a xylM subunit in vitro with (I). The method can be used oxidising a substituted monocyclic aromatic substrate, especially for producing 4-hydroxymethylbenzoic acid, 3-hydroxymethylbenzoic acid, proluic acid, proluic acid, proluic acid, proluicacid producing the producing a companion or 3-methylbenzyl alcohol. The compounds produced are useful as monomers in the production of polyesters used in fibres, films,
                                                                                                                                                                                                                                                                                                                      paints, adhesives and beverage containers. The method is cost-effective and produces fewer environmentally harmful waste products. The present sequence represents xylA isolated from Sphingomonas strain ASU1, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xylene monooxygenase; substituted monocyclic aromatic compound; enzyme; oxidation; biocatalytic; xylM; xylA; 4-hydroxymethylbenzoic acid; p-toluic acid; p-toluic acid; p-toluidalyde; proluidalyde; acid; p-toluidalyde; polyester; 4-methylbenzyl alcohol; m-toluic acid; 3-methylbenzyl alcohol; m-toluic acid; 3-methylbenzyl alcohol; fibre; m-tolualdehyde; paint; adhesive; beverage container.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.9%; Score 123; DB 6; 30.1%; Pred. No. 1.4e-05; ive 20; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sphingomonas pNL1 xylA protein SEQ ID NO:22.
Claim 11; Page 64-65; 70pp; English.
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Best Local Similarity 30.1%
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 346 AA;
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Thomas SM
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                                                                    DU PONT DE NEMOURS & CO
BRAMUCCI M G.
NAGARAJAN V.
                                                                                   Bramucci MG, Nagarajan V,
                                                                                         WPI; 2003-354403/33.
                                                                             THOMAS S M.
                                                                    (DUPO )
(BRAM/)
                                                                          (NAGA/)
```

Oxidizing substituted monocyclic aromatic substrate, by contacting recombinant microorganism having DNA fragment encoding xylene monocxygenase enzyme comprising xylA and xylM subunits, with the

substrate

N-PSDB; ACC49120

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The present introllecture describes a mericou tor contacting a substituted monocyclic arcomatic substrate (I). The method involves contacting a recombinant microorganism comprising a DNA fragment encoding a xylene monocygenase enzyme comprising a xyle subunit and a xylM subunit, with (I), or contacting a xylene monocygenase enzyme comprising a xyle subunit and a xylM subunit in vitro with (I). The method can be used for cydising a substituted monocyclic arcmaric substrate, especially for producing 4-hydroxymethylbenzoic acid, 3-hydroxymethylbenzoic acid, proluic acid, p-tolualdehyde, 4-methylbenzyl alcohol, m-toluic acid, p-tolualdehyde, 4-methylbenzyl alcohol, m-toluic acid, p-tolualdehyde, 4-methylbenzyl alcohol, m-toluic acid, m-tolualdehyde or 3-methylbenzyl alcohol. The compounds produced are useful as monomers in the production of polyesters used in fibres, films, can produce fewer environmentally harmful waste products. The present sequence represents xylA isolated from Sphingomonas pNLI, which is used in an example from the present invention. N. B. The present sequence is not given in the specification, as the specification does not appear to be complete, but is derived from Genbank accession number AF079317 (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; prokaryotic essential gene; cell proliferation; drug design.
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                                                   present invention describes a method for oxidising a substituted
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Xu HH;
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Forsyth RA,
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU41589 standard; protein; 366 AA
                Claim 11; Page; 70pp; English.
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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Best Local Similarity 30.18
Watches 31, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas syringae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zamudio C,
Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 346 AA;
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us-09-430-029-8.rag

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isolate candidate molecules for rational drug discovery programs
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The nivention relates to an isolated nucleic acid compilising any one of the 6213 antisense sequences given in the specification where expression the 6213 antisense sequences given in the specification where expression the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (3) a host cell containing the vector; (3) an isolated or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide, (5) producing the polypeptide; (6) inhibiting cellular contingues acid, (4) an antibody capable of specifically binding the gene product or that has an activity against a biological pathway contiferation or the activity of a gene in an operon required for cuts the gene product or that has an activity against a biological pathway in which a proliferation or the the test compound that inhibits proliferation of an organism acts, (9) manufacturing an antibiotic; (10) profiling a compund's activity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an organism acts, (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed, (12) determining the extent to proliferation of an organism. The attisense nucleic acids are useful for proliferation of an organism. The attisense nucleic acids required for cellular proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, and the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                           The invention relates to an isolated nucleic acid comprising any the 6213 antisense sequences given in the manification.
                                                     claim 25; SEQ ID NO 69513; 1766pp; English
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19.4%; Score 120; DB 6; Length 366; 37.2%; Pred. No. 3.4e-05; Query Match Best Local Similarity Sequence 366 AA;

4,

41; Indels

9; Mismatches

32; Conservative

Matches

284 VEFTDIGKSIRVAPGETVHAAAAKLGLM-IPRACGMGICGTCKVMKLSGEVEM---EHNG 339 10 VIIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRA 69 340 GITDEDVAEGYILSCCSVPKGDVRIE 365 70 HVSAEEENDGYALACRVVPDGDVELE 95 q à δ

ABU40068 standard; protein; 368 AA. (first entry) 19-JUN-2003 ABU40068; RESULT 15 ABU40068

Antisense; prokaryotic essential gene; cell proliferation; drug design. Protein encoded by Prokaryotic essential gene #25595.

Pseudomonas putida.

WO200277183-A2.

03-OCT-2002

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993.

08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Malone Zamudio C, Trawick JD, Ų, Wang

New antisense nucleic acids, useful for identifying proteins or screfor homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. WPI; 2003-029926/02 N-PSDB; ACA43938

screening

Claim 25; SEQ ID NO 67992; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid another acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation, or that inhibits callular proliferation; (8) required for proliferation, or that inhibits callular proliferation; (8) identifying a gene required for callular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which he gene compound; a proliferation or underexpressed; (12) determining the extent product is overexpressed or underexpressed; (12) determining the extent compound; a proliferation of an organism. The antisense nucleic acids required for proliferation to isolate and organism or call activate for proliferation in cells other than S. aureus, S. typhimurium, cells required for proliferation in cells other than S. aureus, S. typhimurium, centent did not form part of the printed specification, but was obtained to proliferation for the sequence is encoded by one of the wipo.int/pub/published_pot_essential genes.

C the target proxerypric essential genes are specification, but was obtained to the content did not form when the content and pot form

Sequence 368 AA;

4; Gaps Length 368; Indels 18.9%; Score 117; DB 6; Lv 40.3%; Pred. No. 7.6e-05; iive 10; Mismatches 29; Query Match 18.9% Best Local Similarity 40.3% Matches 29; Conservative

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24 GESILAGMAKIGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRAHVSABEBENDGYALA 83 300 ð d

CCSVPKGDVRID 367 CRVVPDGDVELE 95 84 à

Search completed: August 5, 2004, 13:15:40 Job time : 57 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model - protein search, OM protein

5, 2004, 13:04:13; Search time 18 Seconds August Run on:

(without alignments) 338.437 Million cell updates/sec

US-09-430-029-8

1 MDAGRVCGTVTIAQTDERYA......RLRKPFFCGMACAGTAAINK 118 619 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Searched:

389414 Total number of hits satisfying chosen parameters: 389414 seqs, 51625971 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:* 5 5 : . . Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 381, App	Sequence 4254, Ap			Sequence 28188, A		7	Sequence 2, Appli	Sequence 2, Appli	Ñ			Sequence 23181, A		Sequence 18, Appl		Sequence 5181, Ap
US-09-198-452A-381	US-09-543-681A-4254	US-09-252-991A-24156	US-09-489-039A-11722	US-09-252-991A-28188	US-09-252-991A-32457	US-09-049-577-2	US-09-390-598-2	US-09-328-553-2	US-09-252-991A-26259	US-09-516-914-21	US-09-489-039A-13838	US-09-252-991A-23181	US-09-347-878-20	US-09-504-358-18	US-09-954-314-18	US-09-134-000C-5181
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91	100	346	840	301	527	144	144	144	172	582	413	9/9	1333	352	352	247
12.2	12.0	12.0	11.9	11.6	11.6	11.4	11.4	11.4	11.4	11.4	11.1	11.1	11.1	11.1	11.1	11.0
75.5	74	74	73.5	72	72	70.5	70.5	70.5	70.5	70.5	69	69	69	68.5	68.5	68
28	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Yano, Tetsuya; No. 64721910tto, Tsuyoshi; Imamura, Takeshi;
APPLICANT: Yano, Tetsuya; No. 64721910tto, Tsuyoshi; Imamura, Takeshi;
APPLICANT: Canon Kabushiki Kaisha
TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,
TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,
TITLE OF INVENTION: Method for Degrading Halogenated Aliphatic Hydrocarbon
TITLE OF INVENTION: Method for Environmental Remediation
TITLE OF INVENTION: Method for Environmental Remediation
GURRENT APPLICATION NUMBER: US/09/453,956
CURRENT APPLICATION NUMBER: US/09/453,956
EARLIER APPLICATION NUMBER: UP P1998-344506
EARLIER PLING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 67.6%; Score 418.5; DB 4;
Best Local Similarity 76.7%; Pred. No. 2e-42;
Matches 79; Conservative 9; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: TomQ polypeptide US-09-453-956-8
                                                    ; Sequence 8, Application US/09453956; Patent No. 6472191; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Ralstonia eutropha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 8
RESULT 1
US-09-453-956-8
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Sequence 2, Application US/09716865
Patent No. 6548292
GENERAL INFORMATION:
APPLICANT: Bramucci, Micheal G
APPLICANT: Nagarajan, Vasantha
APPLICANT: Chen, Mario W.
TITLE OF INVENTION: Bacterial Plasmid Having Genes Encoding Enzymes for the TITLE OF INVENTION: Degradation of Aromatic Compounds US-09-716-865-2 RESULT 2

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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Batent No. 6610836
GENERAL INFORMATION:
APPLICANT GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 TVTIAQTD-ERYACVSGE--SLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 GESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRAH----VSAEEENDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.3%; Score 113; DB 4; Length 39 37.3%; Pred. No. 2.8e-05; ive 12; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Indels
61 ALTPEDREND-VILACASVPLEPCTIDVEPSGLTEEFFSG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 YS---LEADELAAGYVLSCQSLPTSGDVVVDFDAR 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.9%; Score 111; DB 4; 35.8%; Pred. No. 4.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 ISRAHVSAEEENDGYALACRVVP-DGDVELEVAGR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Mismatches
                                                                                                  RESULT 4
18-09-252-991A-17118
Sequence 17118, Application US/09252991A
, Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 ILSCCSVPKGDVVID 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 ALACRVVPDGDVELE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14027
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 35.8%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-489-039A-14027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-17118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                             9 TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR
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                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08499215
Parent No. 5612204
GENERAL INFORMATION:
APPLICANT: Saeki, Hisashi
APPLICANT: Miura, Akira
TITLE OF INVENTION: BIOLOGICAL DEGRADATIVE
TITLE OF INVENTION: TREATMENT OF CHLORINE-SUBSTITUTED ETHYLENE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 AHVSAEBENDGYALACRVVPDGDVELEVAGRIRKPFFCGMACAGTAAINK 118
                                                                                                                                                                                                                                                                                                                                                              .,
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                                                                                                                                                                                                                                                                                                                Query Match 52.0%; Score 322; DB 4; Length 119; Best Local Similarity 56.4%; Pred. No. 7e-31; Matches 62; Conservative 13; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas STREET: 2100 Pennsylvania Avenue CITY: N.W. STATE: Washington D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY. U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Vers:
SOFTWARE: & WordPerfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,215
       FILE REFERENCE: BC1016 US NA
CURRENY PEDLICATION NUMBER: US/09/716,865
CURRENY FILING DATE: 2000-11-26
PRIOR APPLICATION NUMBER: 60/167,062
PRIOR FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP Hei-6-179689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08-JUL-1994
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 342 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39; Conservative
                                                                                                                                                                                                                                             ORGANISM: Pseudomonas CT14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 39; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                               LENGTH: 119
TYPE: PRT
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US-08-499-215-5
                                                                                                                                                                                                                                                                 US-09-716-865-2
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ORGANISM: Acinetobacter baumannii
                   APPLICATION NUMBER: 177,631
FILING DATE: 05-APR-1988
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ORGANISM: Proteus mirabilis
                                                                                                                                       Best_Local Similarity 31.5%
Matches 28; Conservative
 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     US-09-543-681A-7190
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US-09-328-352-6375
                                                                      LENGTH: 326
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                                                                                                                          Query Match
                                                      SEQ ID NO:7
                                                                                      5171684-7
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                                             SALMOND, GEORGE PEACOCK COPELAND
MCGOWAN, SIWON JAMES
SEBAIHLA, WOHAMMED
COX, ANTHONY RICHARD JOHN
HOLDEN, MATTHEW THOMAS GEOFFREY
PORTER, LAUREN ELIZABETH
BYCROFT, BARNE WALSHAM
WILLIAMS, PAUL
STEWART, GORDON SIDNEY ANDERSON BIRNIE
STEWART, GENES INVOLVED IN THE BIOSYNTHETIC PATHWAY OF CARBAPENEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
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MONOXYGENASE OF PSEUDOMANS MENDOCINA KR-1
NUMBER OF SEQUENCES 41
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/590,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.8%; Score 110; DB 2; Length 92; 39.7%; Pred. No. 1e-05; ive 11; Mismatches 25; Indels
                                                                                                                                                                                                          JUNE SEE: Dirch, Stewart, Kolasch & Birch, LLP STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
ZIP....
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,825
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30,330
FR: 1009-0105P
Sequence 7, Application US/08737825
Patent No. 5871922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEGNARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1005
TELEPCOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Erwinia carotovora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Conservative
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                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                               22040-0747
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                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILLING DATE: 03 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
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                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                APPLICANT:
APPLICANT:
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5171684-7
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Sequence 7190, Application US/095436B1A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI)
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT PILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 80/128,706
SEQ ID NOS: 8344
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Betent No. 6562958

GRNERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GT-09-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 358
LENGTH: 358
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                                                                                                                  14 QTDE---RYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRAH 70
                                                                                                                                                     9 TVTIAQTDERYACVSGESLLAGMAKLGRRGIPV--GCLNGGCGVCKVRVLRGAVRKLGPI
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2
     Length 326;
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16.6%; Score 103; DB 4; Length 353;
Best Local Similarity 34.1%; Pred. No. 0.00038;
Matches 30; Conservative 13; Mismatches 37; Indels
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                                                             Indels
16.9%; Score 104.5; DB 6;
31.5%; Pred. No. 0.00023;
tive 16; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                            71 VSAEEENDGYALACRVVPDGDVELEVAGR 99
                                                                                                                                                                                                                                                                  63 LAARELRKNRFLACQCKPLSDLKIKVINR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : ::|:| || ||| |||| ||||| 352 STSTLTADEIAQGYVLACSCRLTGDVEL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 SRAHVSAEEENDGYALACRVVPDGDVEL 94
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Sequence 952, Application US/09198452A
Patent No. 6555294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-99
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
14.7%; Score 91; DB 4; Length 377;
Best Local Similarity 29.7%; Pred. No. 0.011;
Matches 27; Conservative 17; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.6%; Score 90.5; DB 4; 32.5%; Pred. No. 0.015; tive 14; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 EAEKQAAEQH--IALCCSRSLSANLVIDLAG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 RAHVSAEEENDGYALACRVVPDGDVELEVAG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches
                                                                                                                                                      Sequence 9429, Application US/09489039A, Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * |: |: |: | WRLSCQCKVQHDMSLEIEER 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 7, Application US/09453956
                                         321 ADGYVLACSCHPOSDLVL 338
94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 YALACRVVPDGDVELEVAGR
77 NDGYALACRVVPDGDVEL
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Matches 26; Conservative
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                                                                                                                                       US-09-489-039A-9429
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US-09-198-452A-952
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US-09-453-956-7
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Patent No. 6605709
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT PILING DATE: 2000-04-05
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Patent No. 6610836
GENERAL INFORMATION

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: PREMIONIAE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: PREMIONIAE FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1000-01-27

PRIOR PRILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
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                                                                                                                 281 VSVÄQDD------ESILDAALRAG-ADLPYACKGGVCATCRCKVLSGEVDMFLNYS-- 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 DERYACVSGESLIAGMAKLGRRGIPV--GCINGG-CGVCKVRVLRGAVRKLGPISRAHVS 72
                                                                     10 VTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRA
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                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Indels
Best Local Similarity 30.9%; Pred. No. 0.0026; Matches 25; Conservative 12; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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                                                                                                                                                                                           330 -LEEDEVEKGYVLSCOTLPKG 349
                                                                                                                                                                  90
                                                                                                                                                                70 HVSAEEENDGYALACRVVPDG
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32.1%;
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US-09-543-681A-5480
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Best Local Similarity
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Best Local Similarity
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US-09-489-039A-12074
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US-09-543-681A-5480
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LENGTH: 339
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RESULT 15
US-094-489-019A-12111
NS-094-489-019A-12111
Sequence 12111, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFRENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR PILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12111
GENERAL INCORMATION:
GENERAL TITLE OF INVENTION:
FOR INVENTION:
GENERAL FARGMENT FLAND A Fragment Carrying Toluene Monocxygenase Gene,
TITLE OF INVENTION: Method for Degrading Halogenated Alighatic Hydrocarbon
TITLE OF INVENTION: Compounds and Aromatic Compounds, and
TITLE OF INVENTION: Method for Degrading Halogenated Alighatic Hydrocarbon
FILE REPRENCE: CFO140740S
CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: US/09/453,956
CURRENT FILING DATE: 1999-12-03
FARLIER FILING DATE: 1999-12-03
FORWARE: PARCHIER IN OBS: 14
SOFTWARE: PARCHIER IN OBS: 14
SOFTWARE: PARCHIER OF TEACH IN OR: 2.1
FENGURENT FILING DATE: 1990-12-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 GQTILDAALRQGIY-IPHACCHGLCGTCKVSVLDGEA-DLGEANPFALMDFEREEGKALA 76
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Best Local Similarity 34.7%; Pred. No. 0.023;
Matches 25; Conservative 9; Mismatches 36; Indels
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Matches 25; Conservative
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13: \cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: \cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         using sw model
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Gapop 10.0 , Gapext 0.5
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DB seq length: 2000000000
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                                                                                                                                         protein search,
                                                                                                                                                                                                                  August
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Perfect score:
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                                                                                                                                         OM protein
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Maximum |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 8. Appli	Sequence 8 Appli	Seguence 50674, A	Seguence 49233. A	Sequence 47765, A		Sequence 22, Appl	Sequence 12, Appl	Sequence 22, Appl	Sequence 69513, A	Sequence 67992, A	Sequence 66835, A	Sequence 65277, A		
SOMMAKIES	ID	US-09-430-029-8	US-10-223-371B-8	US-10-282-122A-50674	US-10-282-122A-49233	US-10-282-122A-47765	US-10-213-878-12	US-10-213-878-22	US-10-214-059-12	US-10-214-059-22	US-10-282-122A-69513	US-10-282-122A-67992	US-10-282-122A-66835	US-10-282-122A-65277	US-10-282-122A-50897	US-10-424-599-275773
	DB	6	14	12	12	12	14	14	14	14	12	12	12	12	12	12
	% Query Match Length DB	118	111	343	343	343	346	346	346	346	366	368	366	336	348	169
	% Query Match	100.0	67.6	21.1	20.4	20.1	19.9	19.9	19.9	19.9	19.4	18.9	18.3	17.7	17.6	17.0
	Score	619	418.5	130.5	126.5	124.5	123	123	123	123	120	117	113	109.5	109	105.5
	Result No.	-	71	æ	4	ιΩ	9	7	8	σ	10	11	12	13	14	15

18, App 18, App 47415, 142, Ap 68779,	49031, A 65947, A 53556, A 77980, A 111884, A 59569, A	말 그런	133198, 133198, 66811, A 69345, A APD11 31, APD1 44836, A 66819, A
		Sednence Sednence Sednence Sednence Sednence Sednence Sednence Sednence	Sequence 550/4, A Sequence 131198, Sequence 66811, A Sequence 69345, A Sequence 31, Appli Sequence 44836, A Sequence 66819, A Sequence 66819, A
US-10-213-878-18 US-10-214-059-18 US-10-425-114-47415 US-09-738-626-6142 US-10-282-122A-68779	10-282-1 10-282-1 10-282-1 10-282-1 10-282-1 10-282-1	US-10-282-122A-75961 US-10-282-122A-54966 US-10-282-122A-50665 US-10-282-122A-50665 US-10-282-122A-42942 US-10-424-599-150076 US-10-223-371B-7 US-10-289-125-55785	US-110-437-963-13199 US-110-437-963-13199 US-110-282-122A-66811 US-10-282-122A-69345 US-09-430-029-7 US-10-216-464-31 US-110-282-122A-44836 US-110-425-114-6619
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17.0 16.7 16.7 16.6	16.2 16.2 16.3 14.9	44444444 8. 6. 6. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4.	13.7 13.7 13.2 13.0 12.8 12.7
105 103.5 103.5 103.5	101.5 101.5 100 100 94.5 92.5	8 8 9 1000 8 9 1000 6 1000 8 8 8 1000 100 8 8 9	88 84 55 55 55 55 55 55 55 55 55 55 55 55 55
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ALIGNMENTS

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APPLICANT: Yano, Tetsuya; No. US20020168738Aloto, tsuyoshi; Imamura, Takeshi; Canon ]
TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,
TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,
TITLE OF INVENTION: Method for Degrading Chlorinated Aliphatic Hydrocarbon
TITLE OF INVENTION: Compounds and Aromatic Compounds, and
TITLE OF INVENTION: Method for Environmental Remediation
FILE REFERENCE: CF013982US
CURRENT APPLICATION NUMBER: US/09/430,029
CURRENT APPLICATION NUMBER: US/09/430,029
EARLIER APPLICATION NUMBER: UP P1998-310801
EARLIER APPLICATION NUMBER: JP P1998-310801
EARLIER FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDAGRVCGTVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAV
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100.0%; Pred. No. 6.8e-64;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: TomQ polypeptide
                   Sequence 8, Application US/09430029; Patent No. US20020168738Al; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Burkholderia cepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 118; Conservative
US-09-430-029-8
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10 VTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRA 69
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR APPLICATION NUMBER: 60/20/3-20

PRIOR FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/20/335

PRIOR APPLICATION NUMBER: 60/20/335

PRIOR PILING DATE: 2000-09-06

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-29

PRIOR PLING DATE: 2000-10-29

PRIOR PLING DATE: 2000-10-29

PRIOR PLING DATE: 2000-10-2-9

PRIOR PLING DATE: 2001-02-9

PRIOR PLING PLING NUMBER: 60/26/308

PRIOR PLING DATE: 2001-02-9

PRIOR PLING PLING NUMBER: 60/26/308

PRIOR PLING DATE: 2001-02-9

PRIOR PLING DATE: 2001-02-9

PRIOR PLING PLING NUMBER: 60/26/308

PRIOR PLING PLING PRIOR PLING NUMBER: 60/26/308
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                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1 SEQ ID NO 50674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 HVSAEEENDGYALACRVVPDGDVEL---EVAG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 ALSNDERTRGLALLCCSKPOSDLEVDVREIAG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.1%; Score 130.5;
33.7%; Pred. No. 1.5t
iive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 49233, Application US/10282122A ; Publication No. US20040029129A1
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Burkholderia mallei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trawick, John
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Matches 31; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 343
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                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Yano, Tetsuya; No. US20030170877Aloto, Tsuyoshi; Imamura, Takeshi; Canon APPLICANT: Yano, Tetsuya; No. US20030170877Aloto, Tsuyoshi; Imamura, Takeshi; Canon APPLICANT: Kabushiki Kaisha Happliki Hacorganism, Method for Degrading Haloger TITLE OF INVENTION: Aliphatic Hydrocarbon Compounds and Aromatic Compounds, and Methoritie PRILERERENCE: 03500.014074.1
FILE REFERENCE: 03500.014074.1
FULE REFERENCE: 03500.014074.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 TVRVAQTGESFSCTAGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLSGDVRKLGPVSR 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 AHVSAEEENDGYALACRVVPDGDVELEVAGRLRKPFFCGMACA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AHVSADEEGLGYTLACRVAPQGDVELEVAGKMQKPFLC---CA 107
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Pred. No. 1.2e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Mismatches
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mandy, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Chisen, Kari
APPLICANT: Cyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
, OTHER INFORMATION: TomQ polypeptide
US-10-223-371B-8
                                                                                                                Sequence 8, Application US/10223371B Publication No. US20030170877A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 67.6%;
1 Similarity 76.7%;
79; Conservative
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Ralstonia eutropha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
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9 TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR 68
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                                                                                                                                                                                                                                                  10 VIIAQIDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRA 69
                                                                                                                                                                                                                                                                                        APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                              13;
                                                                                                                                                                Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5,
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                                                                                                                                                   Query Match
20.4%; Score 126.5; DB 12; Length
Best Local Similarity 35.4%; Pred. No. 4.4e-06;
Matches 34; Conservative 15; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.1%; Score 124.5; DB 12; Length 32.6%; Pred. No. 7.5e-06; Live 20; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                     70 H----VSAEEENDGYALACRVVPDGDVEL---EVAG 98
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PRIOR DATE: 2003-03-21
PRIOR PILING DATE: 2000-05-33
PRIOR PILING DATE: 2000-05-33
PRIOR PILING DATE: 2000-05-33
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 47765, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                         iENGTH: 343
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
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Best Local Similarity 32.6'
Matches 30; Conservative
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SEQ ID NO 49233
LENGTH: 343
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LENGTH: 343
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APPLICANT:
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APPLICANT:
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US-10-213-878-22

Sequence 22, Application US/10213878

Sequence 22, Application US/10213878

Publication No. US20030073206A1

GENERAL INFORMATION:

APPLICANT: Bramucci, Michael

APPLICANT: Thomas, Stuart

TITLE OF INVENTION: Monocyclic Aromatic Compounds

TITLE OF INVENTION: Monocyclic Aromatic Compounds

FILE REFERENCE: CL1662 US NA

CURRENT APPLICATION NUMBER: US/10/213,878

CURRENT APPLICATION NUMBER: 60/311,490

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Microsoft Office 97

SEQ ID NO 22
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10 VIIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRA 69
                      9 TVTIAQTDERYACVSGESLIAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR 68
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                                                                                                        63 ALSNDERTRGLALLCCSKAQCDLEIDVREIAG 94
                                                                            70 HVSAEEENDGYALACRVVPDGDVEL---EVAG
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; Sequence 12, Application US/10213878
; Publication No. US20030073206A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Sphingomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Sphingomonas sp. US-10-213-878-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 31; Conserv
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Best Local Similarity
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12 TVTVEGSPTTLDIPAGKTLLEAMLDAG-LAMPHDCKVGSCGTCKFKLVSGKIGELSPSAL 70
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LENGTH: 366
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                                                                                                                                                                                                                                                                                     APPLICANT Bramucci, Michael
APPLICANT Bramucci, Michael
APPLICANT Bramucci, Vasantha
APPLICANT Thomas, Stuart
TITLE OF INVENTION: Use of Xylene Monooxygenase for the Oxidation of Substituted
TITLE OF INVENTION: Polycyclic Aromatic Compounds
FILE REPREBUCE: Cle63 US NA
FURENT APPLICATION NUMBER: 00/214,059
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: 60/311,486
PRIOR PILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nagarajan, Vasantha
APPLICANT: Thomas, Studert
TITLE OF INVENTION: Use of Xylene Monooxygenase for the Oxidation of Substituted
TITLE OF INVENTION: Polycyclic Aromatic Compounds
TITLE OF INVENTION: Polycyclic Aromatic Compounds
CURRENT APPLICATION NUMBER: US/10/214,059
CURRENT FILING DATE: 2002-08-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TVTIAQIDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR 68
         12 TVTVEGSPITLDIPAGKTLLEAMLDAG-LAMPHDCKVGSCGTCKFKLVSGKIGELSPSAL 70
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                                                                           69 AHVSAEEENDGYALACRVVPDGDVELEVAGRLRKPFFCGMACA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.9%; Score 123; DB 14; 30.1%; Pred. No. 1.1e-05; iive 20; Mismatches 46;
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PRIOR FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/10214059
Publication No. US20030077768A1
GENERAL INFORMATION:
APPLICANT: Bramucci, Michael
                                                                                                                                                                                                                US-10-214-059-12; Sequence 12, Application US/10214059; Publication No. US20030077768A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
SEQ ID NO 22
LENGTH: 346
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Sphingomonas sp. US-10-214-059-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
, ORGANISM: Sphingomonas sp.
US-10-214-059-12
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Best Local Similarity
Matches 31; Conserv
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US-10-214-059-22
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Best Local &
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TVIIAQIDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR 68

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CURRENT PILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-05-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-06

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PLING DATE: 2000-110-23

PRIOR PLING DATE: 2000-110-23

PRIOR PLING DATE: 2000-110-23

PRIOR PLING DATE: 2000-110-23

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PLING DATE: 2000-110-23

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09
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APPLICANT: Yamamoto, Robert
APPLICANT: Persyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 366;
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                                           69 AHVSAEEENDGYALACRVVPDGDVELEVAGRLRKPFFCGMACA
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Best Local Similarity 37.2%; Pred. No. 2.7e-05;
Matches 32; Conservative 9; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 GITDEDVARGYILSCCSVPKGDVRIE 365
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                                                                                                                                                                                                                                                     Sequence 69513, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Zyskind, Judith
Wall, Daniel
Trawick, John
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US-10-282-122A-67992
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JS-10-282-122A-65277
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APPLICANT:
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                                                                                                                                                                                                                                   APPLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 GESILAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRAHVSAEENDGYALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Indels
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Pred. No. 6.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Mismatches
                                                                                                                                                                                                                                                                FILE REFERENCE: LLITRA,034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66835, Application US/10282122A, Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Chery1
APPLICANT: Malone, Chery1
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Tawick, John
APPLICANT: Trawick, John
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                 R FILING DATE: 2000-03-21

R APPLICATION NUMBER: 60/206,848

R FILING DATE: 2000-05-23

R APPLICATION NUMBER: 60/207,727

R APPLICATION NUMBER: 60/207,727

R APPLICATION NUMBER: 60/230,335

R APPLICATION DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N. FILING DATE: 2000-11-27

DR APPLICATION NUMBER: 60/257,931

DR FILING DATE: 2000-12-22

DR APPLICATION NUMBER: 60/267,636

DR FILING DATE: 2001-02-09

DR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
                                  Wang, Liangsu
: Zamudio, Carlos
: Malone, Cheryl
: Haselbeck, Robert
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US20040029129A1
                                                                                                        Ohlsen, Kari
Syskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 40.35
Matches 29; Conservative
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: G0/191,078

PRIOR APPLICATION NUMBER: 60/202

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/203,35

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-01-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/253,635

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PLING DATE: 2010-02-09

PRIOR PLING DATE: 2010-02-09

PRIOR PLING DATE: 2010-02-09

PRIOR PLING DATE: 2010-02-09

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR APPLICATION NUMBER: 60/269,306

PRIOR APPLICATION NUMBER: 60/
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Best Local Similarity 37.3%; Pred. No. 0.00018;
Matches 28; Conservative 12; Mismatches 25;
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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Publication No. US20040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
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Trawick, John
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US-10-424-599-275773
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LENGTH: 169
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITHA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-66
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
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PRIOR FILING DATE: 2000-09-09
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PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PLILNG DATE: 2000-05-26

PRIOR PLILNG DATE: 2000-05-26

PRIOR PLILNG DATE: 2000-09-06

PRIOR PLILNG DATE: 2000-09-09

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR PLILNG DATE: 2000-110-23

PRIOR PLILNG DATE: 2000-110-23

PRIOR PLILNG DATE: 2000-110-23

PRIOR PLILNG DATE: 2000-110-23

PRIOR PLILNG DATE: 2000-11-27

PRIOR PLILNG DATE: 2000-12-27

PRIOR PLILNG DATE: 2000-12-27

PRIOR PLILNG DATE: 2001-02-09

PRIOR PLILNG DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PRIOR DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PLILNG DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PLILNG DATE: 2001-02-16

PRIOR DATE: 2001-02-16
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Best Local Similarity 30.0%; Pred. No. 0.0004;
Matches 27; Conservative 16; Mismatches 44; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 QALSBAEKAQGKILMCRTTAQSDININIPG 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50897, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
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APPLICANT: Zamudio, Carlos
APPLICANT: Amonio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
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Sequence 275773, Application US/10424599
Publication No. US2004003107241
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-2163233 B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Indels 12; Gaps
                       PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER: 0F SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50897
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Best Local Similarity 40.0%; Pred. No. 0.0005;
Matches 24; Conservative 9; Mismatches 18; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                    17.6%; Score 109; DB 12; Length 348;
29.7%; Pred. No. 0.00048;
tive 16; Mismatches 36; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_91042C.1.pep
US-10-424-599-275773
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APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-10-282-122A-50897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

August Run on:

5, 2004, 13:13:39; Search time 16 Seconds (without alignments) 709.413 Million cell updates/sec

US-09-430-029-8 619 1 MDAGRVCGTVTIAQTDERYA.....RIRKPFFCGMACAGTAAINK 118

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR 78:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		erredoxin [ferredoxin (256-25	erredoxin	erredoxin [2F6-2		xv]ene monocyarens	naphthalene 1 2-di	nhenol hydroxylaso	probable ferredowi	Na+-translocating	probable diomesons	ferredoxin-Nah xed	tolibere_4-monocura	andina transl	Na/./ translocati	na/+/-tailsiocatin		probable Lerredox1		mothers moreth	ferredoxin [250-26	probable oridored:		probable electron	phonol 2 monocurrent		probable oridoxed:	sodium-translocati
SUMMARIES	ΩI	\$16193	B39181	T31266	S24417	4	T46585	T31263	AI2723	E97505	G82970	D64052	A95312	B37316	A47016	D81918	G81184	AG0625	A86451	F81849	AF3320	100000	S75687	A10165	B82094	C70678	S44308	378	953	3
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	Score	195.5	186	172.5	172.5	166.5	129.5	123	114	114	113	112	106		104.5	104	104	102	101.5	101.5	101	100.5	99.5	66	66	66	98	96	98	96
	Result No.	1	71	٣	4	2	9	7	80	σ	10	11		13	14	15	16	17	18	13	20		22						28	29

probable CDP-6-den	probable iron-silf	probable iron	ferredoxin limont	NADH2 dehydrogenes	probable electron	ferredoxin (Shelo	CONSPINED LAFE-23	NADH Oxidored	nara-jeonomy] +o]	ferredoxin 1986-98	ferredoxin [2Ec-23	probable electron	probable election	hymothetical proto	ferredoxin I Atu07
H81091	AC0173	F81100	AH2170	AB0393	C69336	FEDO	H82401	AH0608	JC5499	FEYC2	FEFNG	C64890	G72022	A86601	A12665
N	7	7	N	7	7	Н	7	~	П	П	1	~	2	7	N
336	370	96	122	407	585	93	662	323	349	105	95	356	431	431	360
15.8	15.7	15.6	15.1	15.0	15.0	14.9	14.9	14.8	14.8	14.7	14.6	14.6	14.6	14.6	14.5
97.5	97	96.5	93.5	93	66	92	92	91.5	91.5	91	90.5	90.5	90.5	90.5	90
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT S16193

21913
ferredoxin [2Fe-25]-like protein xvlT - Pseudomonas mitida niamid mumo
C; Species: Pseudomonas putida
 C;Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text Abana 02 no 1000
C; Accession: S16193; S23486
R;Harayama, S.; Polissi, A.; Rekik, M.
FEBS Lett. 285, 85-88, 1991
A;Title: Divergent evolution of chloroplast-type ferredoxins.
A, Reference number: S16193; MUID:91293320; PMID:2065785
A;Accession: S16193
A MOLECULE TYPE: DNA
 A. (Nostunds: 1-112 charts of the control of the control of the charts of the control of the con
 Eur. J. Biochem. 204, 113-120, 1992
A, Title: Cis-diol dehydrogenases encoded by the TOL DWWO plasmid well, nene and the holing
A, Reference number: S23477; MUID: 92155191; PMID: 1740120
A;Accession: S23486
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A;Residues: 1-112 <nei></nei>
A, Cross-references: EMBL:M64747; NID:q151718; PIDN:AAA26051.1: PID:0151703
A, Note: the nucleotide sequence was submitted to the EMBL Data Library March 1992
C;Genetics:
A;Gene: xylT
A;Genome: plasmid pWW0
C;Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology
C; Keywords: 2Fe-2S; electron transfer; iron-sulfur pro; metallonrotein
F;25-82/Domain: ferredoxin [2Fe-2S] homology <fer></fer>
F;41,46,49,81/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
Ouerv Match 31 6%. Grama 106 6. DB 1 1
al Similarity
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26
o data data data data data data data dat
Db 15 QSFRCAEGQSVLRAMEAQGKRCIPVGCRGGGCGLCRVRVLSGAYRS-GRMSRGHVPAKAA 73
Qy 77 NDGYALACRUVPDGDVELE 95
Db 74 AEALALÁCQVFPOTÚLTIE 92

RESULT 2
B19181
B19181
C.Species: Pseudomonas putida
C.Species: D.Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C.Accession: B19181; S16368
R.You, I.S.; Ghosal, D.; Gunsalus, I.C.

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Conservative
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Best Local Similarity
Matches 34; Conserv
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Best Local Similarity
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R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G
submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati
A;Reference number: Z20992
A;Accession: T31266
Biochemistry 30, 1635-1641, 1991
A,Title: Nuclectide sequence analysis of the Pseudomonas putida PpG7 salicylate hydroxyl
A,Reference number: A39181; MUID:91129237; PMID:1993181
                                                                                                 A;Molecule type: DNA
A;Residues: 1-108 <YOU>
A;Cross-references: GB:M60055; GB:J05317; NID:g151380; PIDN:AAA25898.1; PID:g151382
A;Cross-references: GB:M60055; GB:J0517; NID:g151380; PIDN:AAA25898.1; PID:g151382
FEBS Lett. 285; B5-88; 1991
A;Thle: Divergent evolution of chloroplast-type ferredoxins.
A;Reference number: S16193; MUID:91293320; PMID:2065785
A;Accession: S16568
                                                                                                                                                                                                                                                                                                                             A;Residues: 1-108 <hr/>
A;Residues: 1-108 <hr/>
A;Residues: 1-108 <hr/>
A;Residues: 1-108 <hr/>
A;Cross-references: GB:X61466; GB:S40145; NID:g311896; PIDN:CAA43701.1; PID:g311897
C;Superfamily: ferredoxin [2Fe-25], ferredoxin [2Fe-25] homology
C;Reywords: 2Fe-25; electron transfer; iron-sulfur protein; metalloprotein
F;24-81/Domain: ferredoxin [2Fe-25] homology <FER>
F;24-81/Domain: ferredoxin [2Fe-25] homology <FER>
F;40,45,48,80/Binding site: 2Fe-25 cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ferredoxin [2Fe-25]-like protein xylT - Sphingomonas aromaticivorans plasmid pNL1
C,Species: Sphingomonas aromaticivorans
C,Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
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A;Molecule type: DNA
A;Residues: 1-93 <ROM>
A;Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378407; PIDN:AAD03990.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 RYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRAHVSAEEEN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 VTIAQIDERYACVSGESILLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ferredoxin [2Fe-2S]-like protein dmpQ - Pseudomonas putida ferredoxin [2Fe-2S]-like protein dmpQ - Pseudomonas putida C;Species: Pseudomonas putida C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 @Rishingler, V.; Powlowski, J.; Marklund, U.
J. Bacteriol. 174, 711-724, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 186; DB 1; Length 108;
Pred. No. 2.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.9%; Score 172.5; DB 2; 44.3%; Pred. No. 5.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 HVSAEEENDGYALACRVVPDGDVELEVAGRLRKP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 HLPVEAREQGYALACRLFARSDLCIE---RYSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Mismatches
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Best Local Similarity
Matches 35; Conserv
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Best Local Similarity
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A;Gene: xylT
A;Genome: plasmid pNL1
                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                    A; Accession: B39181
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A,Title: Nucleotide sequence and functional analysis of the complete phenol/3,4-dimethy A,Reference number: S24417; MUD:92121108; PMLD:1732207
A,Accession: S24417
A,Accession: S24417
A,Accession: S24417
A,Accession: S24417
A,Residues: 1-112 <SHI>
A,Genecutes: L-112 <SHI>
A,Genecutes: EMBL:X60657; NID:945687; PIDN:CAA43064.1; PID:945688
C,Genetics: A,Gene: dmpQ
C,Superfamily: ferredoxin [2Pe-25]; ferredoxin [2Pe-25] homology
C,Superfamily: ferredoxin [2Pe-25] homology <FRR>
F;25-82/Domain: ferredoxin [2Pe-25] homology <FRR>
F;41,46,49,81/Binding site: 2Pe-25 cluster (Cys) (covalent) #status predicted Cispecies: Pseudomonas putida Cispecies: Pseudomonas putida Cipacies: 03-Dec-1999 #sequence revision 03-Dec-1999 #text_change 03-Dec-1999 Ciaccession: 554762; BS8972; 544309; 847420 Ciaccession: 554762; BS8972; 544309; St7420 RiHerrmann, H.; Mueller, C.; Schmidt, I.; Mahnke, J.; Petruschka, L.; Hahnke, K. RiHerrmann, H.; Mueller, C.; Schmidt, I.; Mahnke, J.; Petruschka, L.; Hahnke, K. AyTitle: Localization and organization of phenol degradation genes of Pseudomonas putid A; Reference number: 554761; MulD:95272534; PMID:7753034 A; Returns nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-101 < HER>
A; Residues: 1-101 < HER>
A; Residues: 1-101 < HER>
A; Cross-references: EmB1:X80765; NID:9527546; PIDN:CAA56746.1; PID:9527553
A; Cross-references: EmB1:X80765; NID:9527546; PIDN:CAA56746.1; PID:9527553
A; More: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
A; More: the nucleotide sequences of C.: Poh, C.L.
Gene 151, 29-36, 1994
A; Title: Cloning and sequences of the first eight genes of the chromosomally encoded A; Reference number: A58972; MUID:95129877; PMID:7828892
A; Accession: B58972 A,Residues: 1-72,'GE', 75-101 <NGL>
A,Residues: 1-72,'GE', 75-101 <NGL>
A,Cross-references: EMBL:X79063; NID:g483477; PIDN:CAA55666.1; PID:g483484
A,Experimental source: strain P35X (NCBI 9869)
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994 ä 1; 16 73 predicted 17 ERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRAHVSAEEE 76 17 ERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRAHVSAEEE C;Superfamily: ferredoxin [2Fe-28]; ferredoxin [2Fe-28] homology C;Keywords: 2Fe-28; electron transfer; iron-sulfur protein; metalloprotein F;25-82/Domain: ferredoxin [2Fe-28] homology <FER> F;41,46,49,81/Binding site: 2Fe-28 cluster (Cys) (covalent) #status predict Gaps 1; Length 101; Length 112; Indels Indels ferredoxin [2Fe-2S]-like protein phlG - Pseudomonas putida 26.9%; Score 166.5; DB 1; 40.0%; Pred. No. 2.2e-09; Artive 17; Mismatches 33; ch 1 Similarity 41.0%; Pred. No. 6.1e-10; 34; Conservative 16; Mismatches 32; 77 NDGYALACRVVPDGDVELEVAGRLR 101 QQGLALACQLYPRADLYIESLRQVR 66 96 77 NDGYALACRVVPDGDVELEVAGR | ||||::| |::| | 74 KQGLALACQLFPQTDLNIECLRR

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Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B., Science 294, 2332-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MuID:21608551; PMID:11743194
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erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Stef. EW.
A; Attlet: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A; Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                     A) Cross-references: GB:AE008688; PIDN:AAL42207.1; PID:g17739599; GSPDB:GN00186
A,Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Superfamily: methane monooxygenase reductase component; cytochrome-b5 reduct
C;Keywords: 2Fe-2S; metalloprotein
F;40,45,48,80/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVTIAQTDERYACVSGESLL----AGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAV--R 61
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C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
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C;Species: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.4%; Score 114; DB 2; Length 337; 33.3%; Pred. No. 0.00098; tive 13; Mismatches 33; Indels
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Best Local Similarity
Matches 31; Conserv
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A;Molecule type: DNA
A;Residues: 1-337 <KUR>
                                                                                                                                                                                                                                        A; Accession: A12723
A; Status: preliminary
A; Molecule type: DNA
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Best Local Simi
Matches 31;
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A;Genome: plasmid pNL1
C;Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolc
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reductase homold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ferredoxin reductase [imported] - Pseudomonas stutzeri
C.Species: Pseudomonas stutzeri
C.Species: Pseudomonas stutzeri
C.Species: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 11-May-2000
C.Accession: T46585
R;Ouchiyama, N.; Miyachi, S.; Omori, T.
G. Gen. Appl. Microbiol. 44, 57-63, 1998
A;Title: Cloning and nucleotide sequence of carbazole catabolic genes from Pseudomonas A;Reference number: 223031
A;Accession: T4658
A;Accession: T4658
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-329 <OUC>
A;Residues: 1-320 <OUC>
A;R
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C; Species: Agrobacterium tumefaciens
C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C; Accession: AI2723
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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A;Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378404; PIDN:AAD03987.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVSGESILLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRAHVSAEEENDGY 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Function: A_1Description: involved in carbazole degradation [validated, PIR:Z231091] C.Superfamily: methane monooxygenase reductase component; cytochrome-b5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.9%; Score 129.5; DB 2; Length 39.0%; Pred. No. 2.9e-05; Live 11; Mismatches 35; Indels
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| A-LEGDELRSGFRIACQAIPRSDLTIAVDA----PLSQGIAIA 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain OM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 39.08
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C;Accession: A95312

K;Barnett, M.J; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow K;Barnett, M.J.; Fisher, R.F.; Jones, T.; Fock, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo A;Teference number: A95262; MUID:21396509; PMID:11481432

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Scatus: preliminary
A;Residues: 1-353 <KUR>
A;Residues: 1-353 <KUR
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: As6039; MUID:21368234; PMID:11474104
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A;Residues: 6-8,'X',10-12,'X',14-16 <SHA>
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37.3%;
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Best Local Similarity 37.3
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Contents: annotation C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S29273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: SMa0752
A;Genome: plasmid
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R.Felschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A. Gocayne, U.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Fitle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: D64052
A;Accession: D64052
A;Accession: D64052
A;Accession: D64052
A;Accession: D64052
A;Accession: D64052
A;Cross-references: GB:U32702; GB:L42023; NID:g1573118; PIDN:AAC21841.1; PID:g1573127; TA;Cross-references: GB:U32702; DB:U42023; NID:g1573118; Covalent; Oxidoreductase
F;58-115/Domain: cytochrome-b5 reductase homology <CBR>F;73,79,82,114/Binding site: 2Fe-25 cluster (Cys) (covalent) #status predicted
                               CyAccession: G82970
RyStower, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, T.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor, A;Accession: G82970
A;Accession: G82970
A;Status: preliminary
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C,Species: Sinorhizobium meliloti
C,Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: GB:AE004953; GB:AE004091; NID:g9951727; PIDN:AAG08796.1; GSPDB:GN001
A,Experimental source: strain FAO1
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A;Gene: PA5411
C;Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferred
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C,Species: Haemophilus influenzae
C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 GESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRAH----VSAEEENDGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.3%; Score 113; DB 2; Length 366; 37.3%; Pred. No. 0.0013; ive 12; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | :|: |: | :|| ||:| | ::|:|: | IL-PTELSHINKREAKEGYRLACQVNVKGNMEVEL 126
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Best Local Similarity
Matches 33; Conserva
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Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                   A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-366 <STO>
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R;Suzuki, M.; Hayakawa, T.; Shaw, J.P.; Rekik, M.; Harayama, S.
J. Bacteriol. 173, 1690-1695, 1991
A;Title: Primary structure of xylene monooxygenase: similarities to and differences from A;Reference number: A37316; MUID:91154124; PMID:1999388
A;Accession: B37316
A;Accession: preliminary
A;Molecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: catalyzes hydroxylation of a methyl side-chain of toluene and xylenes; A;Description: catalyzes hydroxylation of a methyl side-chain of toluene and xylenes; C;Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homo C;Keywords: 2Fe-2S; aromatic hydrocarbon catabolism; FAD; flavoprotein; heterodimer; i F;7-93,Domain: ferredoxin [2Fe-2S] homology <FER> F;121-344/Domain: cytochrome-b5 reductase homology cCBR> F;52,57,60,92/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NyContains: ferredoxin-NAD+ reductase (EC 1.18.1.3) chain A - Pseudomonas putida plasmid pWW0 NyContains: ferredoxin-NAD+ reductase (EC 1.18.1.3) (Species: Pseudomonas putida (Species: Pseudomonas putida C;Date: 01-Oct-1992 #sequence_revision 01-Oct-1992 #text_change 03-Jun-2002 B;Susnit N ....
                                                                                     2;
                                                                                                                                                                                                                             282 CSETDTILAA-AKAAGLVIPSGCSMGICGTCKVRKTEGQVHM---VHNGGITDEDVEDGY 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Residues: 1-350 <SUZ>
A,Residues: 1-350 <SUZ>
A,Cross-references: GB:M37480; NID:g151649; PIDN:AAA26027.1; PID:g151651
R,Shaw, J.P.; Harayama, S.
Bur. J. Biochem. 209, 51-61, 1992
A,Fitle: Purification and characterisation of the NADH: acceptor reductase
A,Reference number: S29273; MUID:93011166; PMID:1327782
                                                                                                                                                                       21 CVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRAHVSAEEENDGY
                                                                                          Gaps
Score 106; DB 2; L. Pred. No. 0.0063; B; Mismatches 35;
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32;
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Job tim
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                                                                                                                                                                                                                                                                                                             RESULT 14
A47016
toluene-4-monooxygenase (EC 1.-..-) reductase component - Pseudomonas mendocina
toluene-4-monooxygenase (EC 1.-..-) reductase component - Pseudomonas mendocina
C;Species: Pseudomonas mendocina
C;Accession: A47016
C;Accession: A47016
C;Accession: A47016
A;Attle: Identification of a new gene, tmoF, in the Pseudomonas mendocina KR1 gene clust
A;Atcession: A47016
A;Accession: A47016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolo C;Keywords: 2Fe-2S; flavoprotein; iron-sulfur protein; metalloprotein; oxidoreductase F;21-77/Domain: ferredoxin [2Fe-2S] homology <FER> F;107-320/Domain: cytochrome-b5 reductase homology <CBR> F;36,41,44,76/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) chain F NMA0747 [simil C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Accession: D81918
C;Accession: D81918
F;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Accession: D81918
A;Status: preliminary
A;Kelerence number: A81775; MUD:20222556; PMID:10761919
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CABB4030.1; PID:g737946
A;Experimental source: serogroup A, strain Z2491
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C;Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homold
C;Keywords: NAD; oxidoreductase
                                                                     2
                                                                                               9 TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR 68
                                                                                                                                14 QTDE---RYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRAH 70
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|SDDLLHHFEADSNDTLLSA-ALRAELVFYECNSGGGACKIELLEGEVSNLWP-DAPG
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: sequence extracted from NCBI backbone (NCBIN:118027, NCBIP:118029)
C;Genetics:
A;Gene: tmoF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-326 <YEN>
A;Cross-references: GB:M95045; NID:g151596; PIDN:AAA26004.1; PID:g151597
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; Pred. No. 0.0082;
16; Mismatches 40; Indels 5
  17.0%; Score 105; DB 2; Length 350; 28.4%; Pred. No. 0.0078; Live 18; Mismatches 43; Indels
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31.5%;
                                                   Conservative
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Matches 28: Consorm
                         Local Similarity
les 25; Conserv
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Query Match
Best Local S:
Matches 25
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8 GTVTIAQTDERYACV-SGESLLAGMAKLGRRGIPVGCLNGG-CGVCKVRVLRGAVRKLGP
                                         Gaps
                                         4;
    DB 2; Length 405; 0.011;
                                     41; Indels
                                                                                                                                            90 TELSHISKREAREGCRLSCQVNVKTDMDIEV 120
16.8%; Score 104; DB
35.2%; Pred. No. 0.01:
live 14; Mismatches
                                                                                                                        66 ISRAHVSAEEENDGYALACRVVPDGDVELEV 96
                               Conservative
Query Match
Best Local Similarity
Matches 32; Consery
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4.

completed: August 5, 2004, 13:17:20

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 5, 2004, 13:09:59; Search time 13 Seconds (without alignments) 472.637 Million cell updates/sec

US-09-430-029-8 619 1 MDAGRVCGTVTIAQTDERYA......RIRKPFFCGMACAGTAAINK 118 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMANTES

	Description). I		P23263 pseudomonas		pseudomona	Ogykan pseudomonas	neisseria	methyloror		m	P19734 Dseudomonas	_	vibrio	l vibrio	versini	7 shewanell				-	3 chlamydia	9		P00230 phytolacca		N	4	ın			Ln.		
SUMMARIES	ID	Transfer State	FERA FORFU	NORF HARTN	XYLA PSEPII		NORF NEIMA	NORF NEIMB	MMOC_METCA	NQRF_PASMU	NORF_VIBCH	DMPP PSESP	NORF VIBAL	NORF_VIBPA	NORF VIBVU	NORF YERPE	NORF SHEPU	FER PERBI	FERZ SYNP6	FER_GLEJA	PAAE ECOLI	NORF CHLPN	NORF_VIBHA	- 1	FER1_PHYES	NORF_COLMA	NORF_VIBPS	HCR_ECOLI		NDOR PSEPU		FER2 EQUTE	NQRF_CHLMU	FER2_EQUAR
	DB	-	٦,	٦,-	٠,	-	П	Н	Н	П	~	Н	Н	Н	Н	П	7	7	Н	Н	Н	Н	-	- Н 1	-4	Н	н.	Н	-1	Н	Н	-4	,	П
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NORF ALTHA	NORF CHICV	FER1 APHFL	FER ARATH	NORF PHOPO	FER2 ARATH	FER SILPR	MOP_DESGI	DMPP ACICA	FER SAMNI	YCBX ECOLI	FER1_SYNP2
Н	-	Н	-	Н	Н	Н	rd	_	Н	Н	н
303	431	97	148	303	148	146	907	352	97	369	96
13.8	13.8	13.7	13.7	13.7	13.6	13.5	13.4	13.2	13.1	13.1	13.0
85.5	85.5	84.5	84.5	84.5	84	83.5	83	81.5	81	81	80.5
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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NORF HAEIN
                                         RESULT 3
NORF HAEIN
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SIMILARITY).
SIMILARITY).
SIMILARITY).

    -!- PATHWAY: Catechol metabolism.
    -!- SIMILARITY: Belongs to the 2Fe2S plant-type ferredoxin family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN=67 / ATCC 17485;

MEDLINE=91129237; PubMed=1993181;

You I.-S., Ghosal D., Gunsalus I.C.;

You I.-S., Ghosal D., Gunsalus I.C.;

"Nucleotide sequence analysis of the Pseudomonas putida PpG7

"Nucleotide sequence analysis of the Pseudomonas putida PpG7

"Ancleotide sequence analysis 
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.0%; Score 186, DB 1; Length 108; 42.6%; Pred. No. 7e-12;
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IRON-SULFUR (2FE-2S) (BY SI
IRON-SULFUR (2FE-2S) (BY SI
IRON-SULFUR (2FE-2S) (BY SI
A; 97B8181EB361574E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=G7 / ATCC 17485;
MEDLINE=91293320; PubMed=2065785;
Harayama S., Polissi A., Rekik M.;
"Divergent evolution of chloroplast-type ferredoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 HVSAEEENDGYALACRVVPDGDVELEVAGRLRKP 103
                                                                                                                                                                                                                                     (Rel. 20, Created)
(Rel. 20, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                      108 AA
                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X61466; CAA43701.1; -.
EMBL; M60055; AAA25898.1; -.
EMBL; B39181; B39181.
InterPro; IPR006058; 2Fe2S fd BS.
InterPro; IPR001041; FerredoxIn.
77 NDGYALACRVVPDGDVELE 95
                                                 74 AEALALACQVFPOTDLTIE 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS Lett. 285:85-88(1991)
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                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48
                                                                                                                                                                                                                                                                                                                        Ferredoxin, plant-type.
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                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=303;
                                                                                                                                                                                                                                        01-NOV-1991
01-NOV-1991
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Best Local Si
Matches 40;
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66 HLPVBAREQGYALACRLFARSDLCIE---RYSKP 96

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                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Na (+)-translocating NaDH-quinone reductase subunit F (EC 1.6.5.-)
(Na (+)-translocating NQR subunit F) (Na (+)-NQR subunit F) (NQR-1 subunit F) (NQR-1 subunit F) (NQR-1 subunit F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS Lett. 381:174-176(1996).

FEBS Lett. 381:174-176(1996).

-!- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by nqrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubisemiquinone by a one-electron transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashi M., Nakayama Y., Unemoto T.; "Existence of Na+-translocating NADH-quinone reductase in Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) = NAD(+) + ubiquinol + Na(+)(Out).
-:- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).
-:- SUBUNIT: Composed of six subunits; ngrA, ngrB, ngrC, ngrD, ngrE and ngrF (By similarity).
-:- SUBCELLOLAR LOCATION: Inner membrane (Potential).
-:- SIMILARITY: Belongs to the ngrF family.
                                                                                                                                                                                                                                                                                       STRAINE-BG / KW20 / ATCC 51907;

STRAINE-BG / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed=7542800;

MEDLINE-95350630; PubMed=7542800;

Reliachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fizzugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R. Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Finchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Ghebh C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001041; Ferredoxin.
InterPro; IPR001709; FPN cyt redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF 00430; -; 1.
InterPro; IPR006058; 2Fe2S fd BS.
InterPro; IPR008333; FAD_binding_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=96176316; PubMed=8601449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U32702; AAC21841.1; -. PIR; D64052; D64052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION AS NOR SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 269:496-512(1995).
  STANDARD;
                                                                                                                                                                                      Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P23486; 1QFJ.
TIGR; HI0171; -
                                                                                                                                                                                                                                                  NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              influenzae.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathway
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PRINTS; PRO0410; PHEHYDRXLASE.
PRO51TE; PS00197; 2FE25 FERREDOXIN; 1.
Aromatic hydrocarbons catabolism; Flavoprotein; Oxidoreductase; FAD; MAD; Metal-binding; Iron-sulfur; Iron; 2Fe-25; Plasmid.

108 FERREDOXIN.
                                                                                                                 HSSP; P06543; ICZP.
InterPro; IPR006058; 2Fe2S fd BS.
InterPro; IPR001834; Cyt B5 reductase.
InterPro; IPR001834; FAD binding 6.
InterPro; IPR001041; Perredoxin.
InterPro; IPR001091; Perredoxin.
                                                                                                                                                                                                                                                               InterPro; IRR001709; FPN cyt redctse.
InterPro; IPR001433; Oxred FAD/NAD(P)
InterPro; IPR001221; Phe_hydroxylase.
                                                                                                                                                                                                                                                                                                                           InterPro; IPR001221; Phe hydroxylan
Pfam; PR00970; FAD binding 6; 1.
Pfam; PR00111; fer2; 1.
Pfam; PR00175; NAD binding 1; 1.
PRINTS; PR00406; CVTBSRDTAŠE.
PRINTS; PR00371; FPNCR.
                            EMBL; M37480; AAA26027.1;
EMBL; D63341; BAA09663.1;
PIR; B37316; B37316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 5
PSEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                               DRAMANA AND BARANA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 GTVTIAQIDERYACV---SGESLLAGMAKLGRRGIPV--GCLNGG-CGVCKVRVLRGAVR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dDITIDINDDPEKAITLPAGGKLLGALAS---KGIFVSSACGGGGSCGOCIVKVKNGGGE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: FAD.
SUBUNIT: COMPOSED OF TWO SUBUNITS: XYLA AND XYLM.
SIMILARITY: IN THE N-TERMINAL REGION WITH 2FE-2S FERREDOXINS, AND IN THE REST OF THE SEQUENCE WITH FERREDOXIN REDUCTASE.
SIMILARITY: TO OTHER BACTERIAL RING-HYDROXYLATING DIOXYGENASE ELECTRON TRANSFER COMPONENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                  CATALYTIC ACTIVITY: Reduced ferredoxin + NAD(+) = oxidized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Xylene moncoxygenase electron transfer component [Includes: Ferredoxin; Ferredoxin--NAD(+) reductase (EC 1.18.1.3)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       82 IRON-SULFUR (2FE-2S) (BY 8
114 IRON-SULFUR (2FE-2S) (BY 8
45705 MW; ED560053E66D23E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                     (BY
(BY
                                                                                                                                                                                                                                                                                                                                                     (2FE-2S)
(2FE-2S)
                                                                                                                                                                                                                             Inner membrane; Complete proteome 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.1%; Score 112; DB 1; 34.7%; Pred. No. 0.00064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 KLGPISRAHVSAEEENDGYALACRVVPDGDVELEV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Mismatches
                                                                                                                                                                                                                                                                                                            CATALYTIC.
IRON-SULFUR (
IRON-SULFUR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 6-16.
                                                                                                                                                                                                                                                                                         FERREDOXIN.
Pfam; PF00970; FAD_binding_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                               120
393
73
79
82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDOXYL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XYLA PSEPU P21394;
                                                                                                                                                                                                                                                TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid
                                                                                                                                                                                                                                                                                                            DOMAIN
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ID XYIA PS

AC P213A-P4

DT 01-MAY-

OC Bacter

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9 TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR 68

69 AHVSAEEENDGYALACRVVPDGDVELEV

96

17.0%; Score 105; DB 1; Length 350; 28.4%; Pred. No. 0.0027;

18; Mismatches

25; Conservative

Gaps

5;

43; Indels

(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).

FERREDOXIN-NADH REDUCTASE.
IRON-SULFUR (2FE-2S) (BY SII
IRON-SULFUR (2FE-2S) (BY SII)

38455 MW;

350 AA;

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Yen K.-M., Karl M.R.;
"Identification of a new gene, tmoF, in the Pseudomonas mendocina KRl
gene cluster encoding toluene-4-monooxygenase.";
J. Bacteriol. 174:7253-7261(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: IN THE N-TERMINAL REGION WITH 2FE-2S FERREDOXINS, AND
                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: ELECTRON TRANSFER COMPONENT OF TOLUENE 4-MONOOXYGENASE
                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Toluene-4-monooxygenase electron transfer component [Includes: Ferredoxin; Ferredoxin-NAD(+) reductase (EC 1.18.1.3)].
                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: FAD.
-!- PATHWAY: Toluene degradation; first step.
-!- SUBUNIT: THE MULTICOMPONENT ENZYME TOLUENE-4-MONOOXYGENASE
IS FORMED BY THE TMOA, TWOB, TWOC, TWOD, TMOE AND TWOF
                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: Reduced ferredoxin + NAD(+) = oxidized
       326 AA
                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 1-14.
   PRT;
                                                                                                                                                                                                                                                         MEDLINE=93054339; PubMed=1429451;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                   ferredoxin + NADH.
                                                                                                                                       Pseudomonas mendocina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLYPEPTIDES
                                                                                                                                                                                         NCBI_TaxID=300;
 PSEME
                                                                                                                                                                                                                                         STRAIN=KR1;
              203304;
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Spratt B.G., Barrell B.G.

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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9KOMB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 QTDE---RYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRAH 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09UVQ3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
(Na(+)-translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=22491 / Serogroup A / Serotype 4A;
MEDLINE=2022556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
IN THE REST OF THE SEQUENCE WITH FERREDOXIN REDUCTASE. SIMILARITY: TO OTHER BACTERIAL RING-HYDROXYLATING DIOXYGENASE ELECTRON TRANSFER COMPONENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
                                                                                                                                                                                                                                                                                                                                                                                                                             16.9%; Score 104.5; DB 1; Length 326; 31.5%; Pred. No. 0.0029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Bečaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Indels
                                                                                                                                                                                                                                                                                                                                            2Fe-2S
                                                                                                                                                                                                                                                                         PRINTS; PRO0371; FPNCR.
PRINTS; PRO0410; PHEHYDRXLASE.
PROSITE; PSO0197; 2FESS FERREDOXIN; 1.
Aromatic hydrocarbons catabolism; Flavoprotein; FAD; Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            405 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 VSAEEENDGYALACRVVPDGDVELEVAGR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 LAARELRKNRFLACQCKPLSDLKIKVINR 91
                                                                                                                                                                                                                                                                                                                                 FERREDOXIN.
                                                                                                                                                                                       InterPro; IPR001041; Ferredoxin.
InterPro; IPR001009; FPN_cyt_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
InterPro; IPR001221; Phe_hydroxylase.
Pfam; PF00970; FAD binding_6; 1.
Pfam; PF00111; fer2; 1.
Pfam; PF00175; NAD_binding_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis (serogroup A)
                                                                                                                                                                    InterPro; IPR006058; 2Fe2S fd BS.
InterPro; IPR008333; FAD_binding_6.
                                                                                                                                                                                                                                                                                                                                                                                                           35983 MW;
                                                                                                                                               EMBL; M95045; AAA26004.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                             PIR; A47016; A47016
                                                                                                                                                                                                                                                                                                                                                                                                           326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subunit F) (NOR
NORF OR NMA0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NORF NEIMA
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEIMA
                                                                                                                                                                                                                                                                                                                                                               METAL
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NORF NE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 GTVTIAQTDERYACV-SGESLLAGMAKLGRRGIPVGCLNGG-CGVCKVRVLRGAVRKLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 GDITIKVNGEKELTMPAGGKLLGALANEG-IFIPSACGGGGSCGOCRVVVKSGGGDIL-P
                                                                                                                                                                                       reduces ubiquinone-1: outliesmiquinone by a one-electron transfer pathway (By similarity).

CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) = NAD(+) +

CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) = NAD(+) +

ubiquinol + Na(+)(Out).

COFACTOR: FAD and a ZFe-2S cluster (By similarity).

SUBUNIT: Composed of six subunits; ngrA, ngrB, ngrC, ngrD, ngrE and ngrF (By similarity).

SUBCELLULAR LOCATION: Inner membrane (Potential).

SINILARITY: Belongs to the ngrF family.
                                                                       -i- FUNCTION: NOR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by ngrF, which accepts electrons from NADH and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Gaps
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport; Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S; Transmembrane; Inner membrane; Complete proteome.
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sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Indels
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E22DC9CFB7B62B0A CRC64;
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CATALYTIC.
IRON-SULFUR (2FE-2S) (1
IRON-SULFUR (2FE-2S) (1
IRON-SULFUR (2FE-2S) (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane; Complete proteome.
24 POTENTIAL.
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PROSITE; PS00197; 2FE2S_FERREDOXIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELSHISKREAREGCRLSCQVNVKTDMDIEV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
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HAMAP; MF 00430; -; 1.
InterPro; IPR001041; Ferredoxin.
InterPro; IPR001041; Ferredoxin.
InterPro; IPR001709; FRN cyt_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF001970; FAD binding_6; 1.
Pfam; PF00111; fer2; 1.
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                                                            Nature 404:502-506(2000).
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387
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                                  meningitidis Z2491."
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Les 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MCSB / Serogroup B, MEDLINE=2017555; PubMed=10710307; Tettelin H., Sanders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Dugherty B.K., Mason T., Clecko A., Parksey D.S., Blair E., Citcone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain
             subunit F) (Na(+)-NQR subunit F) (NQR complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: NOR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by ngrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubisemiquinone by a one-electron transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          usignino. + Na(+) (Out).

COFACTOR: FAD and a 2Fe-2S cluster (By similarity).

SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE and nqrF (By similarity).
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CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) = NAD(+)

ubiquinol + Na(+)(Out).
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INTERPRO; IPRO06058; 2Fe2S fd BS.

INTERPRO; IPRO0833; FAD binding 6.

INTERPRO; IPRO01041; Perredoxin.

INTERPRO; IPRO01043; Oxred FAD/NAD(P).

Pfam; PF00171; far2; 1.

Pfam; PF00175; NAD binding 1; 1.

PROSITE; PS00197; ZFE2S FERREDOXIN, FALSE NEG.

Oxidoreductase; NAD; Ubīquinone; Transport; Sodium transport;

Plawyorrotein; FAD; Meral-binding; Iron; 2Fe-2S;
                                                                                                                                  Neisseria meningitidis (serogroup B).
Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF93BD48FFC2AFCC CRC64;
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CATALTIC.
IRON-SULFUR (2FE-2S) (F
IRON-SULFUR (2FE-2S) (F
IRON-SULFUR (2FE-2S) (7
THEUR (2FE
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TRANSMEM 2 24 POTENTIAL.
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                                                 subunit F) (NQR-1 subunit F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 287:1809-1815(2000)
                                                                                                                                                                                                                        Neisseriaceae; Neisseria.
    (Na(+)-translocating NQR
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TIGR; NMB0564; -.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Mucller J. Lugovskoy A.A., Wagner G., Lippard S.J.;
Monooxygenase reductase and interaction with its hydroxylase.";
Biochemistry 41:42-51 (2002).
-!- FUNCTION: Responsible for the initial oxygenation of methane to methanol in methanols. It also catalyzes the monohydroxylation of a variety of unactivated alkenes, alicyclic, aromatic and heterocyclic compounds. The component C is the iron-sulfur flavoprotein of swMO.
-!- CARINTIC SACTIVITY: Methane + NAD(P)H + O(2) = methanol +
                                 32 GDITIKVNGEKELIMPAGGKLLGALANEG-IFIPSACGGGGSCGOCRVVVKSGGGDIL-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAD(P)(+) + H(2)0.
-!- COFACTOR: Binds 1 2Fe-2S cluster.
-! SUBUNI: The soluble methane monooxygenase (sMMO) consists of four components A/MOOH (composed of alpha/mmoX, beta/mmoX and gamma/mmoZ), B/MMOH (mmoB), C/MMOR (mmoC) and D/MMOD (mmoD).
-!- SIMILARITY: In the N terminal section; belongs to the 2Fe2S plant-
  GTVTIAQTDERYACV-SGESLLAGMAKLGRRGIPVGCLNGG-CGVCKVRVLRGAVRKLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stainthorpe A.C., Lees V., Salmond G.P.C., Dalton H., Murrell J.C., "The methane monooxygenase gene cluster of Methylococcus capsulatus
                                                                                                                                                                                                                                                                                                                                                                                      Methylococcus capsulatus.
Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Methane monooxygenase component C (EC 1.14.13.25) (Methane hydroxylase) (Methane monooxygenase reductase) (Methane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McDonald I., Murrell J.C.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                         | :|:| | :| |:|| | 90 TELSHISKREAREGCRLSCQVNVKTDMDIEV 120
                                                                                66 ISRAHVSAEEENDGYALACRVVPDGDVELEV 96
                                                                                                                                                                                                                                348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 1-16.
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InterPro; IPR001834; Cyt B5_reductase.
InterPro; IPR008333; FAD_binding_6.
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InterPro; IPR001709; FPN cyt redctse.
InterPro; IPR001433; Oxred FAD/NAD(P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90382694; PubMed=2205538;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M90050; AAB62391.2; -.
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                                                                                                                                                                                                                           STANDARD;
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Gaps

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41; Indels

16.8%; Score 104; DB 1; Length 405; 35.2%; Pred. No. 0.004;

Pred. No. 0.004;

14; Mismatches

Conservative

Best Local Similarity Matches 32; Conserv

Query Match

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send an email to license@isb-sib.ch)
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16-OCT-2001 (
16-OCT-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 İLTAVTEDGESLIRFECRSDEDVITAAL---RONİFLMSSCREĞĞCATCKALCSEĞDYDLK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
(Na(+)-translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genomic sequence of Pasteurella multocida Pm70.";
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-: FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to
ubiquinol by two successive reactions, coupled with the transport
of Na(+) ions from the cytoplasm to the periplasm. The first step
is catalyzed by ngrF, which accepts electrons from NaDH and
reduces ubiquinone-1 to ubisemiquinone by a one-electron transfer
pathway (By similarity).
-: CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) = NAD(+) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 TVTIAQTDE---RYACVSGESLLAGMAKLGRRGIPV--GCLNGGCGVCKVRVLRG----
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ubiquinol + Na(+)(Out).
COFACTOR: FAD and a 2Fe-2S cluster (By similarity).
SUBUNIT: Composed of six subunits; ngrA, ngrB, ngrC, ngrD, ngrE
                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
                       Pfam; PF00111; fer2; 1.
Pfam; PF00111; fer2; 1.
Pfam; PF00111; fer2; 1.
PRINTS; PR00406; CYTESRDTAŠE.
PRINTS; PR00406; CYTESRDTAŠE.
PRINTS; PR00410; PHENTENDALASE.
PROSITE; PS00197; ZFE2S FERREDOXIN; 1.
CXidoreductase; Monooxygense; NADP; One-carbon metabolism; Electron transport; Metal-binding; Iron-sulfur; Iron; ZFE-2S; Flavoprotein; FA); 3D-structure.
METAL.
42 42 TRON. our print of the carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and carbon and car
                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 348;
                                                                                                                                                                                                                                                                                                                     FAD (NAD PART) (BY SIMILARITY). 7577BEB408CA1C1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      16.2%; Score 100.5; DB 1; Length 3, 30.0%; Pred. No. 0.0077; Live 12; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and ngrF (By similarity).
SUBCELLULAR LOCATION: Inner membrane (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 --AVRKLGPISRAHVSAEEENDGYALACRVVPDGDVELEV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 GCSVQALPP-----EEEEEGLVLLCRTYPKTDLEIEL 94
                                                                                                                                                                                                                                       IRON-SULFUR (2FE-2S).
IRON-SULFUR (2FE-2S).
IRON-SULFUR (2FE-2S).
IRON-SULFUR (2FE-2S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the ngrF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 AA
               InterPro; IPR001221; Phe_hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                          ilarity 30.0%; Pr
Conservative 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                 348 AA; 38541 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subunit F) (NQR-1 subunit F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasteurella multocida.
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                                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity
                                                                                                                                                                                                                                                                                50
82
221
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9CLAG;
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                                                                                                                                                                                                                                                                                         METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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STRAINEEL TOR N16961 / Serotype O1;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey B.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I6-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Na(+)-translocating NaDH-quinone reductase subunit F (EC 1.6.5.-)
(Na(+)-translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR-1 subunit F) (NQR-1 subunit F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 GTVTIAQTDERYACV---SGESILAGMAKLGRRGIPV--GCLNGG-CGVCKVRVLRGAVR
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SIMILARITY).
SIMILARITY).
SIMILARITY).
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MEDLINE=9917036; PubMed=10077658;
Haese C.C., Mekalanos J.J.
"Effects of changes in membrane sodium flux on virulence gene
                                                                                                                                                                                                                                                                                                           Oxidoreductase, NAD; Ubīquinone; Transport; Sodium transport; Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S; Transmembrane; Inner membrane; Complete proteome.

24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9DAC403C9662C8C3 CRC64;
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(BY
(BY
(BY
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(2FE-2S)
(2FE-2S)
(2FE-2S)
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Proc. Natl. Acad. Sci. U.S.A. 96:3183-3187(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | :|:| | :::|:
89 IL-PTELSHISKREAKEGYRLSCQVNVKNSMKVEL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 KLGPISRAHVSAEEENDGYALACRVVPDGDVELEV 96
                                                                                                                                                                                                                                                                     PRINTS; PR00371; FPNCR.
PROSITE; PS00197; 2FE2S_FERREDOXIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.6%; Pred. M. 32.6%; Aive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRON-SULFUR (IRON-SULFUR (IRON-SULFUR (
                                                                                                                                                                                                                                                                                                                                                                                                               FERREDOXIN.
CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRON-SULFUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.2%; Score 100;
                                        HAMME, MF 00430; -; 1.
InterPro; IPR006058; 2Fe2S fd BS.
InterPro; IPR0060333; FAD binding_6.
InterPro; IPR001041; Ferredoxin.
InterPro; IPR001433; Oxred FAD/NAD(P).
Pfam; PF00970; FAD binding_6; 1.
Pfam; PF00171; fer2; 1.
Pfam; PF00175; NAD_binding_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
EMBL; AE006171; AAK03417.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45252 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                 116
389
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75
78
110
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75
78
110
407 AA;
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10 VTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISRA
         component).
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METAL
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       SOLITIE TO THE TRANSPORT OF THE TOTAL TO THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF
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                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by ngrF, which accepts electrons from NDH and reduces ubiquinone-1 to ubisemiquinone by a one-electron transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 GIVIIA-QIDERYACVS--GESLLAGMAKLGRRGIPVGCLNGG-CGVCKVRVLRGAVRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phenol hydroxylase P5 protein (BC 1.14.13.7) (Phenol 2-monooxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                          CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) = NAD(+) + ubiquinol + Na(+)(Out).

COFACTOR: FAD and a 2Fe-2S cluster (By similarity).

SUBUNIT: Composed of six subunits; ngrA, ngrB, ngrC, ngrD, ngrE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC.
IRON-SULFUR (2FE-2S) (BY SIMILARITY)
IRON-SULFUR (2FE-2S) (BY SIMILARITY)
IRON-SULFUR (2FE-2S) (BY SIMILARITY)
IRON-SULFUR (2FE-2S) (BY SIMILARITY)
               "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.0%; Score 99; DB 1; Length 408; 34.4%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 IRON-SULFUR (2FE-2S) (BY 8
45066 MW; F5665E9623CAAD7B CRC64;
                                                                                                                                                                                                                                                  and ngrF (By similarity).
SUBCELLULAR LOCATION: Inner membrane (Potential).
SIMILARITY: Belongs to the ngrF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inner membrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - PTELDHISKGEAREGERLACQVAVKADMDLEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPISRAHVSAEEENDGYALACRVVPDGDVELEV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.4%; Preu. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
FERREDOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF117331; AAD29967.1; -. EMBL; AE004300; AAF95434.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Conservative
                                                   Nature 406:477-483 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
1117
390
70
76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; B82094; B82094.
HSSP; P33007; 1B9R.
TIGR; VC2290; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111
408 AA;
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273
70
76
79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
TRANSMEM
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ID DMPP_PSESP
AC P19734;
DT 01-FEB-1991
DT 01-FEB-1991
DT 15-MAR-2004
DE Phenol hydro
                                                                                                                                                                pathway
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SEQUENCE
                                  cholerae
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by P0, P1, P2, P3, P4 and P5 polypeptides.
-!- SIMILARITY: In the N-terminal section; belongs to the 2Fe2S plant-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91072231; PubMed=2254259;
Powlowski J., Shingler V.;
Fowlowski J., Shingler V.;
In vitro analysis of polypeptide requirements of multicomponent phenol hydroxylase from Pseudomonas sp. strain CF600.";
J. Bacteriol. 172:6834-6840(1990).
-! FUNCTION: Catabolizes phenol, and some of its methylated derivatives. PS is required for growth on phenol, and for in vitro phenol hydroxylase activity.
-! FUNCTION: Probable electron transfer from NADPH, via FAD and the ZPe-2S center, to the oxygenase activity site of the enzyme.
-!- CATALYTIC ACTIVITY: Phenol + NADPH + O(2) = catechol + NADPE(+) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: P5 contains a FAD cofactor and a ferredoxin-type 2Fe-2S
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-!- PATHWAY: Phenol biodegradation; first step.
-!- SUBUNIT: The multicomponent enzyme phenol hydroxylase is formed
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Flavoprotein; FAD; NADP; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
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IRON-SULFUR (2FE-2S) (BY SIMILARITY)
IRON-SULFUR (2FE-2S) (BY SIMILARITY)
IRON-SULFUR (2FE-2S) (BY SIMILARITY)
                                                                                                                                                                                                 MEDLINE=91072230; PubMed=2254258; Nordlund I., Powlowski J., Shingler V.; "Complete nucleotide sequence and polypeptide analysis of multicomponent phenol hydroxylase from Pseudomonas sp. strain
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InterPro; IPR006058; ZFe2S fd BS.
InterPro; IPR001834; Cyt B5_reductase.
InterPro; IPR001831; FAD_binding_6.
InterPro; IPR001041; Ferredoxin.
InterPro; IPR001221; Phe hydroxylase.
Pfam; PF00111; fer2; Interpro; PF00111; fer2; InterPro; PF00111; fer2; InterPro; PR00410; FAD binding_6; I.PRIMYS; PR00410; PHEHYDRXLASE.
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seudomonas sp. (strain CF600).
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HSSP; P00235; 1FRR.
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                                Plasmid pVI150.
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"Expression and analysis of the gene for the catalytic beta subunit of
the sodium-translocating NADH-ubiquinone oxidoreductase of Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakayama Y., Hayashi M., Unemoto T., "Identification of six subunits constituting Na+-translocating NADH-quinone reductase from the marine Vibrio alginolyticus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20016049; PubMed=10549856; Nakayama Y., Hayashi M., Yoshikawa K., Mochida K., Unemoto T.; Nakayama Y. Hayashi M., Yoshikawa K., Mochida K., Unemoto T.; Inhibitor studies of a new antibiotic, korormicin, 2-n-heptyl-4-hydroxyquinoline N-oxide and Ag+ toward the Na+-translocating NADH-quinone reductase from the marine Vibrio alginolyticus."; Biol. Pharm. Bull. 22:1064-1067(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unemoto T., Ogura T., Hayashi M., "Modifications by Na+ and K+, and the site of Ag+ inhibition in the Na+-translocating NADH-quinone reductase from a marine Vibrio
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=95246889; PubMed=7729558;
Hayashi M., Hirai K., Unemoto T.;
Hayashi M., Hirai K., Unemoto T.;
"Sequencing and the alignment of structural genes in the ngr operon encoding the Na(+)-translocating NADH-quinone reductase from Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=DSM 2171;
MEDLINE=98055703; PubMed=9395325;
Steuber J., Krebs W., Dimroth P.;
"The Na+-translocating NADH:ubiquinone oxidoreductase from Vibrio alginollyticus -- redox states of the FAD prosthetic group and mechanism of Ag+ inhibition.";
                                                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
(Na(+)-translocating NADH-quinone reductase subunit beta) (Na(+)-translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR complex subunit F) (NQR-1 subunit F) (NQR-1 subunit F)
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MEDLINE=96230452; PubMed=8674603;
Tan K., Beattie P., Leach D.R.F., Rich P.R., Coulson A.F.W.,
                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
                                                                                                                          407 AA
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                                       70 HVSAEEENDGYALACRVVPDGDVELE
                                                       PRT;
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MEDLINE=98149659; PubMed=9490015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett. 422:240-242(1998)
                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 363:75-77(1995).
                                                                                                                           STANDARD;
                                                                                                                                                                                                                                               Vibrio alginolyticus.
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Blochim. Biophys. Acta 1505:45-56(2001).

Lichard Biochim Biophys. Acta 1505:45-56(2001).

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                         Hayashi M., Nakayama Y., Unemoto T.;
"Recent progress in the Na'+)-translocating NADH-quinone reductase
from the marine Vibrio alginolyticus.";
Biochim. Biophys. Acta 1505:37-44(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ubiquinol + Na(+)(Out).
COFACTOR: FAD and a 2Fe-2S cluster (Probable).
ENZYME REGULATION: ACTIVATED BY NA(+) OR K(+). INHIBITED
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Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron;
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PROSITE, PS00197; 2FE2S_FERREDOXIN; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FERREDOXIN.
CATALYTIC.
IRON-SULFUR
IRON-SULFUR
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IRON-SULFUR
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InterPro; IPR006058; 2Fe2S fd BS.
InterPro; IPR001041; Ferredoxin.
InterPro; IPR001041; Ferredoxin.
InterPro; IPR001709; FPN cyt redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P)
MEDLINE=21145117; PubMed=11248187;
                                                                                                                                                                                                                                                                                MEDLINE=21145118; PubMed=11248188;
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Pfam; PF00175; NAD_binding_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00970; FAD_binding_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB008030; BAA22915.1; -.
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407 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathway.
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                                                                                                                                                                                                                                                                                                                                   Steuber J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32
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                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
(Na(+)-translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR-1 subunit F)
NQRF OR NQR6 OR VP2346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kato S., Yumoto I.; "Detection of the Na(+)-translocating NADH-quinone reductase in marine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Can. J. Microbiol. 46:325-332(2000).

-!-FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by ngrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubisemiquinone by a one-electron transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=RIMD 2210633 / Serotype 03:K6;
MBDLINE=22508454; PubMed=12620739;
MRAKINO K., OSHIME K., KUXOKAWE K., YOKOYAME K., Uda T., Tagomori K.,
Iijime Y., Najime M., Nakano M., Yamashite A., Kubota Y., Kimura S.,
Yasuunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTOR: BD and a 2Fe-2S cluster (By similarity).
SUBUNIT: Composed of six subunits; ngrA, ngrB, ngrC, ngrD, ngrB and ngrF (By similarity).
SUBCELDULAR LOCATION: Inner membrane (Potential).
SIMILARITY: Belongs to the ngrF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathway.
CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) = NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRIGHTS; FROUS.1; FEBNE.
PROSITE; PSOUS.1; FEBNE.
Oxidoreductase; NAD; Ubīquinone; Transport; Sodium transport;
Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
-PTELDHITKGEAREGERLACQVAMKTDMDIEL 122
                                                                                                                                                    407 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP005081; BAC60609.1; -
EMBL; BA024725; BAA83762.1; -
HAWAP; MF 00430; -; 1.
InterPro; IPR006058; 2Pe2S fd BS.
InterPro; IPR001041; Ferredoxin.
InterPro; IPR001041; Ferredoxin.
InterPro; IPR001709; FPN cyt redctse.
InterPro; IPR001433; Oxred FAD/NAD(P).
Ffan; Pr00970; FAD binding_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20242140; PubMed=10779868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00111; fer2; 1.
Pfam; PF00175; NAD binding 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacteria using a PCR technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 72-374 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ubiquinol + Na(+)(Out)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lancet 361:743-749(2003).
                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00371; FPNCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=JCM 2147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=670;
                                                                                                                                                 VIBPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 1
                                                                                RESULT NAME OF COORDINATE OF C
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                    8 GTVTIA---QIDERYACVSGESLLAGMAKLGRRGIPVGCLNGG-CGVCKVRVLRGAVRKL 63
                                                                                                                                                                                                                                                                                                                              GDITISVNGDADKAIVTQPGGKLLSALAGAG-VFVSSACGGGGSCGQCRVKVKSGGGDIL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
(Na(+)-translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR complex subunit F) (NQR-1 subunit F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - FUNCTION: NOR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by ngrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubisemiquinone by a one-electron transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Composed of six subunits; ngrA, ngrB, ngrC, ngrD, ngrE
                                                                                    SIMILARITY).
SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathway (By similarity).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) = NAD(+)
ubiquinol + Na(+)(Out).
-!- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                         Length 407;
                                                                                                                                                                                                                                                                        42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of Vibrio vulnificus CMCP6."; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                           1 -> V (IN KEF. 2).
GLA -> MLQ (IN REF. 2).
747DCC8E99EDBE3A CRC64;
                                                                    (BY
(BY
(BY
(BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and ngrF (By similarity).
SUBCELLULAR LOCATION: Inner membrane (Potential).
                                                                  (2FE-2S)
(2FE-2S)
(2FE-2S)
(2FE-2S)
 Complete proteome.
                                                                                                                                 V -> M (IN REF. 2)
Q -> E (IN REF. 2)
I -> V (IN REF. 2)
                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                            0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.
                                                                                                                                                                                                                                                                      16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the ngrF family.
                                                                                                                                                                                                                                                                                                                                                                       64 GPISRAHVSAEEENDGYALACRVVPDGDVELEV
                                                                  IRON-SULFUR
IRON-SULFUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407
                                                                                                   IRON-SULFUR
IRON-SULFUR
                                 FERREDOXIN. CATALYTIC.
                                                                                                                                                                                                                                     15.5%; Score 96; 31.2%; Pred. No.
membrane;
                                                                                                                                                                                                      45083 MW;
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HAMAP; MF_00430; -; 1.
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                  69
75
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185
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 Inner
                                                                                                                                                                                                407 AA;
                                                                                                                                                                                                                                                     Similarity
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Fransmembrane;
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Best Local Simi.
Matches 29;
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               RANSMEM
                                                                                                                                                    CONFLICT
                                                                                                                                                                                                    SEQUENCE
                                                                                                                                 CONFLICT
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NORF VIBVU
                                                                                                                 METAL
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89 IL-PTELSHISKREAKEGCRLACOVNVKONLKIEL 122
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10-OCT-2003 (Rel. 42, Last annotation update)
Na (+) -translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
(Na (+) -translocating NQR subunit F) (Na (+) -NQR subunit F) (NQR-1 subunit F) (NQR-1 subunit F).
NQRP OR YPO3235 OR Y0956.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CO-92 / Biovar Orientalis;
STRAIN=CO-92 / Biovar Orientalis;
BEBLINE=11470413; DubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A. Davies R.W., Davies P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.";
Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol. 184:4601-4611(2002).

- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTVTIA---QTDERYACVSGESLLAGMAKLGRRGIPVGCLNGG-CGVCKVRVLRGAVRKL
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(BY SIMILARITY).
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InterPro; 12.

InterPro; 1PR001041; Fel.

InterPro; 1PR001043; Oxred FAL/.

InterPro; 1PR001043; InterPro; Inter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.5%; Score 96; DB 1; Length 407; 31.2%; Pred. No. 0.025; tive 16; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 -PIELDHITKGEAREGERLACQVAVKTDMDIEL 122
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28-FEB-2003 (Rel. 41, Last seq
10-OCT-2003 (Rel. 42, Last ann
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reduces ubiquinone-1 to ubisemiquinone by a one-electron transfer pathway (By similarity).

PATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) + ubiquinol + Na(+) (Out).

COFACTOR: FAD and a 2Fe-2S cluster (By similarity).

SUBUNIT: Composed of six subunits; ngrA, ngrB, ngrC, ngrD, ngrE and ngrF (By similarity).

SUBCETLULAR LOCATION: Inner membrane (Potential).

SIMILARITY: Belongs to the ngrF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Gaps
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catalyzed by ngrF, which accepts electrons from NADH and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport
Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
Transmembrane; Inner membrane; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 15.0%; Score 93; DB 1; Length 407; Local Similarity 30.5%; Pred. No. 0.05; nes 29; Conservative 17; Mismatches 39; Indels
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75 IRON-SULFUR (2FE-2S) (BY S
78 IRON-SULFUR (2FE-2S) (BY S
110 IRON-SULFUR (2FE-2S) (BY S
45455 MW; 24AEFDA035483136 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00311; FPNCR.
PROSITE; PS00197; 2FE2S_FERREDOXIN; FALSE_NEG.
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InterPro; IPR006058; 2Fe2S fd BS.
InterPro; IPR001041; Ferredoxin.
InterPro; IPR001041; Ferredoxin.
InterPro; IPR00143; Oxred FAD/NAD(P).
Pfam; PF00910; FAD binding_6; 1.
Pfam; PF00111; fer2; 1.
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Search completed: August 5, 2004, 13:16:03

OM protein - protein search, using sw model

August 5, 2004, 13:13:04; Search time 38 Seconds (without alignments) 979.767 Million cell updates/sec Run on:

619
1 MDAGRVCGTVTIAQTDERYA.....RLRKPFFCGWACAGTAAINK 118 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

US-09-430-029-8

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL 25:* Database

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*

sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_crganelle:* vertebrate:* unclassified:* sp_bacteriap:* sp_phage:*
sp_plant:*
sp_rodent:* rvirus:* sp virus:* 55. 77. 77. 77. 77. 77. 77. 77. 77. 77. Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:

SUMMARIES

comamonas s pseudomonas comamonas t Q8vut6 burkholderi burkholderi Description Q9ae71 Q9s144 Q9znp1 Q9rb86 Q9zan6 Q9AE71 Q9S144 Q9SNP1 Q9EXM1 Q9EXM1 Q9BB90 Q93JX0 Q84964 Q9RAF3 Q8VUT6 Q9RB86 9NAZ 60 Length DB Query Score Result No.

0;

Gaps

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Length 118;

Score 426; DB 2; Length 11 Pred. No. 3.3e-35; 9; Mismatches 21; Indels

68.8%; ilarity 72.7%; Conservative

Query Match Best Local Similarity Matches 80; Conserv

9 9

1 MDAGRVCGTVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAV

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pseudomonas burkholderi

pseudomonas sphingomona

Q45344 Q847G8 Q9Z3W9

pseudomonas escherichia pseudomonas

burkholderi

082817 pseudomonas 053527 pseudomonas 055701 pseudomonas 085701 pseudomonas 085701 pseudomonas 085105 pseudomonas 024827 acinetobact 052302 rhodococus 07405 cycloclasti 08xwn9 raistonia s 032476 pseudomonas 0814 pseudomonas 0810 janthinobac 08571 sphingomona 07vspl bordetella 08818 pseudomonas 08618 pseudomonas 07w375 bordetella 08410 pseudomonas 07w375 bordetella 08410 pseudomonas 07w375 bordetella 08418 pseudomonas 07w375 bordetella 089183 pseudomonas 07w375 bordetella 089183 speudomonas 07w375 bordetella 089183 speudomonas 098183 speudomonas 07w375 bordetella 089183 speudomonas 098183 speudomonas 098183 rhizobium 1 0913v4 pseudomonas 098013 rhizobium 1 0913v4 pseudomocar	OBUTTG OBUTTG
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1817 1974 1974 1974 1061 1061 1078 1028 1028 1038	PRT; 1. Created) Last seque: Last annotice. C. Tast annotice. T.; Advoxlase of Advoxlase of transporter transporter transport; Trans
082817 085974 085974 088009 08KUV5 08KLV5 022167 052106 024827 052108 0732824 086111 0708P1 0865971 0708P1 086818	20, Created) 20, Last sequesty, Last annomer bhkG. s. s. ata Y.; ata Y.; l hydroxylase the EMBL/GenB ton transporte ron transporte con transporte e25 fd BS. FERREDOXIN; 1 22 MW; 0F694F
	rel. 20, Cre cel. 20, Las cel. 25, Las cel. 25, Las cel. 25, Las nsis. ceria; Betap urkholderia. cond hydrox cond bydrox cond
1101 1103 1103 1103 1103 1103 1103 1103	ULT 1 OBVUTC OBVUTC OBVUTC OBVUTC OBVUTC OLOMAR-2002 (TERBILEL 20, La OLOCT-2003 (TERBILEL 25, La Ferredoxin-like protein PhkG. PHKG. Burkholderia kururiensis. Bacteria, Proteobacteria, Beta Burkholderiaceae, Burkholderia NCBI TAXID-89498; (1) SEQUENCE FROM N.A. SEQUENCE FROM N.A. "Involvement of a phenol hydro, in TCE degradation.", Submitted (JUN-2001) to the EM Submitted (JUN-2001) to the EM EMBL; ABOR3252; BAB79285.1 GO; GO:0005489; F:electron traa InterPro; IPRO0059; F:electron traa InterPro; IPRO01041; Ferredoxil PROSITE; PS00197; ZFE2S_FERRED INCH: Iron: SUDILUIT. SEQUENCE 118 AA; 12492 MW;
2000 2000 2000 2000 2000 2000 2000 200	OBUTTG OBUTTG OBUTTG OBUTTG OLOMAR-2002 (TEMBLEEL) OLOCT-2003 (TEMBLEEL) OLOCT-2003 (TEMBLEEL) PETCEDOXIN-LIKE PROTEINEL BUTKHOLDERIA PROTEINERS SEQUENCE FROM N.A. SEBUNG ABURDA SEBUNG ABURDA INVOLVEMENT OF ABURDA SERUMINER (UNN-2001) TO SEMBL, ABOG3252; BEDF928 GO; GO:0005189; F:electt GO:0006189; F:electt THEFFRO; IPROG059; ZF INTERPRO; IPROGO59; ZF INTERPROSILE; PSOG197; ZFE25;
	002 003 003 in-11 FRO FRO FRO 0051 1 PP 00611 1 PP 00611
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1 MDAGRVCG--TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRG 58
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MEDLINE=97144524; PubMed=8990291;
MEDLINE=97144524; PubMed=8990291;
Michimori F., Saint C.P.;
"Nucleotide sequences and regulational analysis of genes involved conversion of aniline to catechol in Pseudomonas putida UCC22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pukumori F., Saint C.P.;
"Aniline degradation in Pseudomonas putida UCC22(pTDN1): Initial characterization of its conversion to catechol.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
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0
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                                                                                           Length 123;
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                                                                                                                         25; Indels
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                                                                123 AA; 12981 MW; DAD2753277BBD586 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D85415; BAB62044.1; -. GO; GO:0046821; C:extrachromosomal DNA; IEA. GO; GO:0005489; F:electron transporter activity; IEA. GO; GO:0005418; P:electron transport; IEA. InterPro; IPR006058; 2Fe2S fd BS. InterPro; IPR01041; Ferredoxin.
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Best Local Similarity 63.2%; Pred. No. 1.1e-28;
Matches 74; Conservative 9; Mismatches 26.
                                                                                           59.0%; Score 365; DB 2; 63.2%; Pred. No. 4.7e-29; iive 14; Mismatches 25;
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PROSITE; PS00197; ZFEZS_FERREDOXIN; 1.
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                      Pfam; PF00111; fer2; 1.
PROSITE; PS00197; 2FE2S_FERREDOXIN;
Iron; Iron-sulfur.
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          IPR001041; Ferredoxin.
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01-OCT-2001 (TrEMBLrel. 18,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-29 FROM N.A.
                                                                                                            Similarity 63.28
                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas putida.
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             InterPro;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                     Teramoto M., Futamata H., Harayama S., Watanabe K.; "Characterization of a high-affinity phenol hydroxylase from Comamonas testosteroni R5 by gene cloning, and expression in Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                             Comamonas testosteroni (Pseudomonas testosteroni).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Comamonadacea; Comamonas.
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Comamonadaceae; Comamonas.
NCBI_TaxID=285;
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MEDLINE=99018839; PubMed=9802031;
Arai H., Akahira S., Ohishi T., Maeda M., Kudo T.;
"Adaptation of Comamonas testosteroni TA441 to utilize phenol: organization and regulation of the genes involved in phenol degradation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                              aeruginosa PAOIC.";
Mol. Gen. Genet. 262:552-558(1999).
-!- COPACTOR: BINDS 1 2FE-2S CLUSTER (BY SIMILARITY).
BMBL, ABO24741; BAA874.1;
GO; GO:0005489; F:=lectron transporter activity; IEA.
GO; GO:0006118; P:=lectron transport; IEA.
InterPro; IPR006058; 2Fe2S fd BS.
InterPro; IPR001041; Ferredoxin.
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-!- COFACTOR: BINDS 1 2FE-2S CLUSTER (BY SIMILARITY).
EMBL; AB006479; BAA34175.1; -.
GO; GO:0005489; F:=lectron transporter activity; IEA.
GO; GO:0006118; P:=lectron transport; IEA.
InterPro; IPR006058; 2Fe2S fd BS.
InterPro; IPR001041; Ferredoxin.
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64.6%; Pred. No. 7.4e-25;
live 12; Mismatches 22;
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PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
                                                      Created)
           PRT;
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MEDLINE=20055761; PubMed=10589844;
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                         Q9S144;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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         PRELIMINARY;
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                                                                                                                                                                                   Gaps
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"Conversion of 3-chlorocatechol by various catechol 2,3-dioxygenases
and sequence analysis of the chlorocatechol dioxygenase region of
psudomonas putida GJ31.",
J. Bacteriol. 181:1309-1318(1999).
-I-COPACTOR: BINDS 1 22E-2S CLUSTER (BY SIMILARITY).
BMB.; AR109307; AAD05249.1; ...
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005489; F:electron transport; IEA.
InterPro; IPR001041; Ferredoxin.
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Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 52.2%; Score 323; DB 2; Length 121; l Similarity 64.6%; Pred. No. 7.6e-25; Conservative 12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.0%; Score 322; DB 2; Length 119; Best Local Similarity 56.4%; Pred. No. 9.4e-25; Matches 62; Conservative 13; Mismatches 35; Indels
                                                                       121 AA; 12722 MW; C29F512A8BDCC749 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                    70 HVSAEEENDGYALACRVVPDGDVELEVAGRLRKPFF 105
                                                                                                                                                                                                                                                                                                                                                     119 AA
Pfam; PF00111; fer2; 1.
PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
Iron, Iron-sulfur.
SEQUENCE 121 AA; 12722 MW; C29F512.
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Iron; Iron-sulfur.
SEQUENCE 119 AA; 12747 MW; 12256BE
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                                                                                                                                               Local Similarity
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SEQUENCE FROM N.A.
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10 VIIAQIDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGA-VRKLGPISR 68
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"Phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties.";
microbiology 144:0-0(0).
-! COFACTOR: BINDS 1 2FE-2S CLUSTER (BY SIMILARITY).
EMBL; AF026065; AAC32458.1; -.
                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales;
Pseudomonadaceae, Pseudomonas.
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Burkholderiaceae, Ralstonia.
NCBI_TaxID=67939;
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:000618; P:electron transport; IEA.
InterPro; IPR006058; ZFe25 fd BS.
InterPro; IPR001041; Perredoxin.
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Last annotation update)
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Last annotation update)
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55.3%; Pred. No. 2.6e-19;
iive 15; Mismatches 24
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                                         70 HVSAEEENDGYALACRVVPDGDVELEVAGRLRK 102
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PROSITE; PF00111; fer2; 1.
Iron; Iron-sulfur; Plasmid.
SEQUENCE 111 AA; 11919 MW; 0F51741
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MEDLINE=98361023; PubMed=9695910;
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Best Local Similarity 55.00
Each 252; Conservative
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01-OCT-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murrakami S., Nakanishi Y., Kodama N., Takenaka S., Shinke R., Aoki K.;
"Purification, characterization, and gene analysis of catechol 2,3-
dioxygenase from the aniline-assimilationg Pseudomonas species AW-2.";
Biosci. Biotechnol. Biochem 62:747-752(1998).
EMBL; AB004065; BAB18932.1;
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR00608; ZPe2S, fd BS.
InterPro; IPR001041; Ferredoxin.
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                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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"Conserved and hybrid meta-cleavage operons from PAH-degrading
Burkholderia RP007.";
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0
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Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.3%; Score 286.5; DB 2; Length 109; llarity 60.2%; Pred. No. 3.2e-21; Conservative 11; Mismatches 25; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                           48.8%; Score 302; DB 2; Length 91;
64.7%; Pred. No. 7.2e-23;
ive 12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 AA; 11618 MW; 7AB11FA560333E39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF112136; AAF02425.1; -...
GO; GO: 0005449; F:electron transporter activity; IEA.
GO; GO: 0005118; P:electron transport; IEA.
InterPro; IPR006058; 2Fe25 fd BS.
InterPro; IPR001041; FerredoxIn.
Pfam; PF00111; ferz; 1.
PROSITE; PS00197; 2FE25_FERREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 262:308-314(1999).
                                                                                                                                                                                                                                                                                                                        Pfam; PF00111; fer2; 1.
PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
SEQUENCE 91 AA; 9529 MW; BCF548719F903C5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 DVELEVAGRIRKPFFCGMACAGTAA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PVNLEVACKLSKPFSKGRAESATAS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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MEDLINE=99382283; PubMed=10448110;
                                                                                                                       TRANSPOSON=Tn5-Mob;
MEDLINE=98276889; PubMed=9614705;
                                       Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chloroplast-type ferredoxin.
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Best Local Similarity 64...
Best Local Similarity 64...
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burkholderia sp. RP007
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SEQUENCE 109 AA:
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                                                                                                        FROM N.A
                 Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
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SEQUENCE 1
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Best Local 9
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Q9RB90; Q9RB90

SON BRANCH STREET STREE

RESULT 9 Q9RB90

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Gaps 3;

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17 ERYACVSGESILAGMAKLGRRGIPVGCLNGGCGVÇKVRVLRGAVRKLGPISRAHVSAEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Park D.-W., Kim Y., Lee S.-M., Ka J.-O., Kim C.-K.;
"Cloning and Sequence Analysis of the xyll Gene Responsible for 4CBA-bibydrodiol Dehydrogenase from Pseudomonas sp. S-47.";
J. Microbiol. 38:275-280(2200).
                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.2%; Score 205.5; DB 2; Length 112; 49.4%; Pred. No. 4.5e-13; Live 14; Mismatches 25; Indels 1.
                                                                                                                                                                                                                                                             PERK D.-W., Kim C.-K.;

PEARK D.-W., Kim C.-K.;

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

BMBL, AF320981, AAKO8203.2, -

GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:0005489; F:electron transport; IEA.

InterPro; IPRO06058; FFe2S fd_BS.

InterPro; IPRO06058; FFE2S fd_BS.

InterPro; IPRO01041; Ferredoxin.

Pfam; PF00111; fer2; 1.

PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.

SEQUENCE 112 AA, 12054 MW; 799D4F0D3EBAE226 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         112 AA; 12054 MW; 799D4F0D36EAE226 CRC64;
           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                         Probable plant-type ferredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 AEGFALACQVFPQTDLTIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                       NCBI_TaxID=115714;
                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                             Sp.
                                                                                        Pseudomonas
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01-NOV-1996
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                                                                                                                                                                                                                    9 TVTIAQTDERYACVSGESILAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLGPISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TVEIAGSGQCYPCAPEQNLLRAMEALGKRGIPAGCRGGGCGVCKVRIEAGRYH-TGKMSR
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"Constitutive trichloroethylene degradation led by tac promoter chromosomally integrated upstream of phenol hydroxylase genes of Ralstonia sp. KN1 and its nucleotide sequence analysis.";
J. Biosci. Bioeng. 89:47-54(2000)

EMBL, AB031996; BA84124.1;

HSSP; P56408; 1AMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
NCBI_TaxID=103439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                         36.9%; Score 228.5; DB 2; Length 101; 48.9%; Pred. No. 2e-15; Live 12; Mismatches 35; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     th 35.1%; Score 217.5; DB 2; Length 115; I Similarity 45.7%; Pred. No. 2.9e-14; 43; Conservative 14; Mismatches 36; Indels 1;
                                                                                                                          101 AA; 10833 MW; 7A7E2A53B831C15D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 AA; 12319 MW; BB696BF26DD97721 CRC64;
             GO; GO:0005489; F:electron transporter activity; IEA. GO; GO:0006118; P:electron transport; IEA. InterPro; IPR006058; 2Fe2S fd BS. InterPro; IPR001041; Perredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO, GO:0005499; F:electron transporter activity; IBA. GO; GO:0006118; P:electron transport; IEA. InterPro; IPR00658; 2Fe2S fd BS. InterPro; IPR001041; Ferredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                 69 AHVSAEEENDGYALACRVVPDGDVELEVAGRLRK 102
                                                                                                                                                                                                                                                                                                      69 AHVSAEEENDGYALACRVVPDGDVELEVAGRLRK 102
                                                                                                                                                                                                                                                                                                                                                                                                     115 AA
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PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
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PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
Iron, Iron-sulfur.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                       46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ferredoxin-like protein.
                                                                                                                                                      Query Match
Best Local Similarity
HSSP; P56408; 1AWD
                                                                                                           Iron, Iron-sulfur.
SEQUENCE 101 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=KN1;
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Kukor J.J., Olsen R.H.;
"Catechol 2,3-dioxygenases functional in oxygen-limited (hypoxic)
environments.";
                                                                                             Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                         Pfam, PF00111; fer2; 1.
PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
Iron: Iron-sulfur.
SEQUENCE 119 AA; 13024 MW; 12552001D304F8CE CRC64;
                                                                                                                                                                                                                                                        Appl. Bnviron. Microbiol. 62:1728-1740(1996).
-1- COFACTOR: BINDS 1 2FE-2S CLUSTER (BY SIMILARITY).
BMBL: U20258, AAC13786-1; -1.
GO: GO: 00005489; F:electron transporter activity; IEA.
GO; GO: 0006518; P:electron transport; IEA.
InterPro; IPR006058; 2Fe2S fd BS.
InterPro; IPR011041; Ferredoxin.
                                        01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
    119 AA.
                             Created)
  PRT;
                                                                                                                                                                                                  MEDLINE=96209237; PubMed=8633871;
                            (TrEMBLrel. 01, (TrEMBLrel. 01,
                                                                     Chloroplast-type ferredoxin.
PRELIMINARY;
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112 AA

PRT;

PRELIMINARY;

Q9ANS9; Q9ANS9

Q9ANS9 ID Q9 AC Q9

us-09-430-029-8.rspt

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                                                                                                                                                                                         28 LIGMLRIGRKGIPVGCVNGGCGVCKVRVLDGSTR-LGRRQPCPRQRRRKSA----GLTL 81
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Pseudomonas putida.
Plasmid pDTG1.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=303;
Query Match 32.9%; Score 203.5; DB 2; Length 119; Best Local Similarity 51.0%; Pred. No. 7.7e-13; Matches 49; Conservative 6; Mismatches 30; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Explairs G.J., Dennis J.J.;

"Complete nucleotide sequence of the NAH plasmid pDTG1 from "Complete nucleotide sequence of the NAH plasmid pDTG1 from Pseudomonas putida NCIB 9816-4.";

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF491307; AA064306.1; -.

GO; GO:0046821; C:extrachromosomal DNA; IEA.

GO; GO:004689; F:electron transporter activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR006058; 2Fe2S fd BS.

InterPro; IPR001041; Ferredoxin.
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Best Local Similarity 42.6%; Pred. No. 1.9e-11;
Matches 40; Conservative 16; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 AA; 11344 MW; 48568FAC91D640BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Perredoxin.
                                                                                                                                                                                                                                                                                               83 ACRVVPDGDVELEVAGRIRKPFFCGMACAGTAAINK 118
                                                                                                                                                                                                                                                                                                                                                 28 LAGMAKLGRRGIPVGCLNGGCGVCKVRVLRGAVRKLG---
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PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
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SEQUENCE FROM N.A.
STRAIN=NCIB 9816-4;
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2847G8
1D Q847G
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